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OM protein - protein search, using sw model

Run on: October 21, 2002, 16:09:50 ; Search time 31 Seconds
(without alignments)
756.018 Million cell updates/sec

Title: US-09-817-814-2
Perfect score: 1118
Sequence: 1 MAPAEVGGFLGLEGLGQQ.....PRPVDPERVPELYKDLIMYT 211

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802.*
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20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1118	100.0	211	21	AAB18635 Amino acid sequenc
2	1118	100.0	211	22	AAU09931 Human fibroblast g
3	1118	100.0	211	22	AAU09931 Human fibroblast g
4	1118	100.0	211	22	AAU02081 Human fibroblast g
5	1118	100.0	211	22	AAU02081 Human fibroblast g
6	1074	96.1	212	22	AAU02080 Human fibroblast gro
7	778.5	69.6	220	18	AAW11548 Amino acid sequenc
8	774.5	69.3	208	13	AAU02707 Glia activating fa
9	774.5	69.3	208	13	AAU02713 Glia activating fa
10	774.5	69.3	208	15	AAU056505 Glia activating fa
11	774.5	69.3	208	16	AAU080784 Fibroblast growth

12	774.5	69.3	208	16	AAU080784 FGF-9. Homo sapie
13	774.5	69.3	208	18	AAW11547 Amino acid sequenc
14	774.5	69.3	208	19	AAW57519 Fibroblast growth
15	774.5	69.3	208	19	AAW53024 Fibroblast growth
16	774.5	69.3	208	21	AAU10299 Fibroblast growth
17	774.5	69.3	208	21	AAU10299 Human FGF-9 protei
18	774.5	69.3	208	21	AAU0418 FGF-9, SEQ ID NO:1
19	774.5	69.3	208	21	AAU0418 Human fibroblast g
20	774.5	69.3	208	21	AAU0418 Human fibroblast g
21	774.5	69.3	208	22	AAU0418 Murine fibroblast
22	774.5	69.3	208	22	AAU0418 Human fibroblast g
23	774.5	69.3	208	22	AAU0418 Human fibroblast g
24	774.5	69.3	208	22	AAU0418 Human fibroblast g
25	774.5	69.3	208	22	AAU0418 Human fibroblast g
26	774.5	69.3	208	22	AAU0418 Human fibroblast g
27	774.5	69.3	208	22	AAU0418 Human fibroblast g
28	769.5	68.8	207	15	AAU0418 Human fibroblast g
29	758.5	67.8	205	13	AAU0418 Glia activating fa
30	758.5	67.8	205	15	AAU0418 Glia activating fa
31	758.5	67.8	206	13	AAU0418 Glia activating fa
32	758.5	67.8	206	13	AAU0418 Glia activating fa
33	758.5	67.8	206	15	AAU0418 Glia activating fa
34	742	66.4	175	15	AAU0418 Glia activating fa
35	742	66.4	176	15	AAU0418 Glia activating fa
36	742	66.4	177	13	AAU0418 Glia activating fa
37	742	66.4	178	13	AAU0418 Glia activating fa
38	729	65.2	159	15	AAU0418 Glia activating fa
39	729	65.2	160	15	AAU0418 Glia activating fa
40	708.5	63.4	207	20	AAU0418 Human FGF-16 prote
41	708.5	63.4	207	21	AAU0418 Human fibroblast g
42	708.5	63.4	207	22	AAU0418 Human fibroblast g
43	708.5	63.4	207	22	AAU0418 Human fibroblast g
44	708.5	63.4	207	22	AAU0418 Human fibroblast g
45	705.5	63.1	207	20	AAU0418 Rat FGF-16 protein

ALIGNMENTS

RESULT 1
AAB18635
ID AAB18635 standard; Protein; 211 AA.
XX
AC AAB18635;
XX
DT 22-JAN-2001 (first entry)
XX
DE Amino acid sequence of human fibroblast growth factor (FGF)-20.
XX
KW PD10-VEGFuc; gene delivery vector; eye disease; neovascular disease;
KW neurotrophic factor; anti-angiogenic factor; eye disease; glaucoma;
KW macular degeneration; diabetic retinopathy; retinitis pigmentosa;
KW inherited retinal degeneration; surgery-induced retinopathy;
KW retinal detachment; photic retinopathy; toxic retinopathy;
KW trauma-induced retinopathy; wet age related macular degeneration;
KW ARMD; retinopathy; fibroblast growth factor-20; FGF-20.
XX
OS Homo sapiens.
XX
PN WO2000054813-A2.
XX
PD 21-SEP-2000.
XX
PF 15-MAR-2000; 2000WO-US07062.
XX
PR 15-MAR-1999; 99US-0124460.
PR 06-JAN-2000; 2000US-0174984.
XX
(CHIR) CHIRON CORP.
PA (REGC) UNIV CALIFORNIA.
XX
PI Manning WC, Dwarki VJ, Rendahl K, Zhou S, McGee LH, Lau D;
PI Flannery JG, Miller S, Wang F, Di Polo A;

XX WPI: 2000-618862/59.
DR N-PSDB; AAA75630.
XX
PT Treating or preventing eye diseases or inhibiting neovascular disease
PT of the eye, comprises intraocularly administering a gene delivery
PT vector that directs expression of neurotrophic factors or
PT anti-angiogenic factors -
XX
PS Disclosure: Fig 29; 86pp; English.
XX
CC The present sequence represents human fibroblast growth factor (FGF)-20.
CC FGF-20 is expressed using a gene delivery vector of the invention.
CC Vectors of the invention are used for treating or preventing eye
CC diseases, or inhibiting neovascular disease of the eye. The gene
CC delivery vector directs the expression of one or more neurotrophic
CC factors, or anti-angiogenic factors, such that the disease of the eye
CC is prevented or treated. The gene delivery vectors are useful for
CC treating or preventing diseases of the eye such as macular degeneration,
CC diabetic retinopathy, inherited retinal degeneration such as retinitis
CC pigmentosa, glaucoma, surgery-induced retinopathy, retinal detachment,
CC photic retinopathy, toxic retinopathy or trauma-induced retinopathy and
CC for inhibiting neovascular diseases such as wet age related macular
CC degeneration (ARMD) or retinopathy of prematurity.
XX
SQ Sequence 211 AA;
Query Match 100.0%; Score 1118; DB 21; Length 211;
Best Local Similarity 100.0%; Pred. No. 2.9e-111;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPLAEVGGFLGGLGQQVGSFLLPAGERPPLLGERRSAARSARGPGAAQLAHL 60
DB 1 MAPLAEVGGFLGGLGQQVGSFLLPAGERPPLLGERRSAARSARGPGAAQLAHL 60
QY 61 HGILRRQLYCRTFHQLQILPDGSGVQGTRODHSFLGILEFISVAVGLVIRGVDGLYL 120
DB 61 HGILRRQLYCRTFHQLQILPDGSGVQGTRODHSFLGILEFISVAVGLVIRGVDGLYL 120
QY 121 MNDKGLYGSEKLTSECIFRQGFENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA 180
DB 121 MNDKGLYGSEKLTSECIFRQGFENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA 180
QY 181 SKRHQKTFHLPVPDPERVPELYKDLLMYT 211
DB 181 SKRHQKTFHLPVPDPERVPELYKDLLMYT 211
RESULT 2
AAU09931
ID AAU09931 standard; Protein; 211 AA.
XX
AC AAU09931;
XX
XX 15-JAN-2002 (first entry)
XX
XX Human fibroblast growth factor-like (FGF-L) polypeptide sequence.
XX
XX Human; fibroblast growth factor-like; FGF-L; agonist; antagonist;
KW vulnary; virucide; hepatotropic; antiinflammatory; gut disorder;
KW hepatitis; diabetes; wound healing; ulcer; liver disorder;
KW lung disorder; angiogenesis.
XX
XX Homo sapiens.
XX
XX WO200168854-A2.
XX
XX 20-SEP-2001.
XX
XX 13-MAR-2001; 2001WO-US08013.
XX
XX 13-MAR-2001; 2000US-188786P.
XX
XX

PA (AMGE-) AMGEN INC.
XX
PI Jing S, Bass MB;
XX
DR WPI: 2001-596910/67.
DR N-PSDB; AAS15701.
XX
XX New fibroblast growth factor-like polypeptide and polynucleotide for
PT diagnosis, prevention and treatment of diseases, disorders or
PT conditions involving the central nervous system, teeth, heart, liver or
PT adipose tissue -
XX
PS Claim 3; Fig 1; 116pp; English.
XX
CC The present invention relates to new isolated fibroblast growth
CC factor-like (FGF-L) nucleic acid molecules and polypeptides. The FGF-L
CC polypeptide is useful for determining whether a compound inhibits FGF-L
CC polypeptide, and also for identifying a compound that binds to the
CC polypeptide. The FGF-L polypeptides of the invention are useful for
CC treating, preventing or ameliorating a medical condition or an FGF-L
CC polypeptide-related disease, condition or disorder such as wound healing
CC disorders, ulcers, gut disorders, lung disorders, liver disorders such as
CC hepatitis and diabetes. The invention is also useful for diagnosing a
CC pathological condition or susceptibility to a pathological condition in
CC a subject and is useful for modulating levels of FGF-L in an animal.
CC other uses are detecting or quantifying the amount of FGF-L polypeptide
CC and for identifying or developing novel agonists and antagonists of the
CC FGF-L polypeptide signalling pathway which are useful for treating one
CC or more diseases or disorders, and also as an immunogen for producing
CC antibodies for in vivo imaging. The present sequence encodes the human
CC FGF-L polypeptide of the invention. The present sequence represents the
CC human FGF-L polypeptide of the invention.
XX
SQ Sequence 211 AA;
Query Match 100.0%; Score 1118; DB 22; Length 211;
Best Local Similarity 100.0%; Pred. No. 2.9e-111;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPLAEVGGFLGGLGQQVGSFLLPAGERPPLLGERRSAARSARGPGAAQLAHL 60
DB 1 MAPLAEVGGFLGGLGQQVGSFLLPAGERPPLLGERRSAARSARGPGAAQLAHL 60
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DB 61 HGILRRQLYCRTFHQLQILPDGSGVQGTRODHSFLGILEFISVAVGLVIRGVDGLYL 120
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DB 121 MNDKGLYGSEKLTSECIFRQGFENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA 180
QY 181 SKRHQKTFHLPVPDPERVPELYKDLLMYT 211
DB 181 SKRHQKTFHLPVPDPERVPELYKDLLMYT 211
RESULT 3
AAG65666
ID AAG65666 standard; protein; 211 AA.
XX
AC AAG65666;
XX
XX 07-JAN-2002 (first entry)
XX
XX Human fibroblast growth factor (FGF)-20.
XX
XX Fibroblast growth factor; FGF; FGF-like polypeptide; mitogenic;
KW fat deposition; vulnary; antiulcer; dermatological; anorectic;
KW antidiabetic; antiinflammatory; cytostatic; hepatic; virucide;
KW neuroprotectant; pulmonary; gene therapy; vaccine; human.
XX
XX Homo sapiens.
XX

PN WO200172957-A2.
XX 04-OCT-2001.
XX 02-APR-2001; 2001WO-IB00664.
XX 31-MAR-2000; 2000US-0540118.
XX (ITOH/) ITOH N.
XX Itoh N;
XX WPI; 2001-611623/70.
XX New human nucleic acid encoding fibroblast growth factor-like peptide,
PT useful for treatment and diagnosis of e.g. wounds and inflammatory
PT bowel disease -
XX
XX Disclosure; Fig 3; 172pp; English.
XX The invention provides human nucleic acids encoding fibroblast growth
CC factor (FGF)-like peptide. The FGF-like polypeptides can be expressed by
CC standard recombinant methodology and are mitogenic for a wide range of
CC cells, inducing differentiation and proliferation, and inhibiting
CC deposition of fat. The FGF-like polypeptides, polynucleotides and
CC specific antibodies and modulators are useful for treating a very wide
CC range of diseases and conditions, e.g. wounds, ulcers, skin aging,
CC obesity, diabetes, alopecia, inflammatory bowel disease, emphysema, viral
CC hepatitis, multiple sclerosis, respiratory distress syndrome, tumors of
CC the eye, etc., also for maintaining organs before transplant and
CC supporting culture of primary cells and tissues. Sequences AAG5647-67
CC represent amino acid sequences of some members of the FGF family.
XX
XX Sequence 211 AA;
XX
Query Match 100.0%; Score 1118; DB 22; Length 211;
Best Local Similarity 100.0%; Pred. No. 2.9e-111;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPLAEVGGFLGGLEGVGSHFLLPPAGERPPLLGERRSAERSARGGPGAAQLAHL 60
DB 1 MAPLAEVGGFLGGLEGVGSHFLLPPAGERPPLLGERRSAERSARGGPGAAQLAHL 60
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DB 121 MNDKGLYSEKLTSCIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGR 180
QY 181 SKRHQKFTFLPRPDPVPERVPELYKDLLMYT 211
DB 181 SKRHQKFTFLPRPDPVPERVPELYKDLLMYT 211
RESULT 4
AAU02081
ID AAU02081 standard; Protein; 211 AA.
XX
AC AAU02081;
XX
DT 07-SEP-2001 (first entry)
XX
DE Human fibroblast growth factor 20, FGF-20.
XX
KW Human; fibroblast growth factor 20; FGF-20; Parkinson's disease;
KW substantia nigra; dopaminergic neuron; cochlea-associated disease;
KW otosclerosis; Cogan's syndrome; Meniere's disease; Pendred's syndrome;
KW diabetes-associated hearing loss; congenital malformations;
KW autoimmune disease-related hearing loss; age-related hearing loss;
KW deafness; ischaemia-related hearing disturbance; immunogen;
KW antibody; neuro-degenerative disease; tendonitis; wound healing;

KW stroke; ischaemia.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 170..186
FT Binding-site /label= Heparin_binding_site
XX
XX WO200131008-A2.
PN
XX 03-MAY-2001.
XX 20-OCT-2000; 2000WO-US29237.
XX 22-OCT-1999; 99US-0161162.
PR 08-MAR-2000; 2000US-0187856.
XX (CHIR) CHIRON CORP.
PA (KYOU) UNIV KYOTO.
XX
XX Itoh N, Kavanaugh WM;
XX WPI; 2001-308642/32.
DR N-PSDB; AAS03277.
XX
XX New human and rat Fibroblast Growth Factor (FGF) polypeptides for
PT providing trophic support for cells used in Parkinson patients, and
PT alleviating brain and cochlea conditions -
XX
XX Claim 12; Fig 8; 73pp; English.
XX The sequence is Human fibroblast growth factor 20, FGF-20. The FGF
CC polypeptides and nucleic acids encoding them are useful for providing
CC trophic support for cells in a patient, especially a patient with
CC Parkinson's disease, and FGF-20 is additionally used to treat patients
CC with conditions of the substantia nigra. The polypeptides and nucleic
CC acids are useful for alleviating human brain conditions by slowing
CC degeneration, restoring function of, or increasing the number of,
CC dopaminergic neurons. The polypeptides and nucleic acids are also
CC useful for alleviating cochlea-associated disease by slowing of the
CC degeneration of or restoring or maintaining normal function of the
CC structure of cochlea, where the disease is otosclerosis, Cogan's
CC syndrome, Meniere's disease, Pendred's syndrome, diabetes-associated
CC hearing loss, congenital malformations, autoimmune disease-related
CC hearing loss, age-related hearing loss, deafness associated with lack
CC of FGF receptor and ischaemia-related hearing disturbance. Other
CC diseases thought to be amenable to FGF therapeutic activity include
CC neuro-degenerative diseases, tendonitis, wound healing, stroke and
CC ischaemia. The polypeptides can be used to screen for agonists and
CC antagonists. Epitope bearing fragments of the FGF-20 polypeptides can be
CC used to raise anti-FGF-20 antibodies.
XX
XX Sequence 211 AA;
XX
Query Match 100.0%; Score 1118; DB 22; Length 211;
Best Local Similarity 100.0%; Pred. No. 2.9e-111;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPLAEVGGFLGGLEGVGSHFLLPPAGERPPLLGERRSAERSARGGPGAAQLAHL 60
DB 1 MAPLAEVGGFLGGLEGVGSHFLLPPAGERPPLLGERRSAERSARGGPGAAQLAHL 60
QY 61 HGILRRQLYCRGTFHQLQILPDGSGVQGTRODHSFLFGILEFISVAVGLVSRGVDGLYL 120
DB 61 HGILRRQLYCRGTFHQLQILPDGSGVQGTRODHSFLFGILEFISVAVGLVSRGVDGLYL 120
QY 121 MNDKGLYSEKLTSCIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGR 180
DB 121 MNDKGLYSEKLTSCIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGR 180
QY 181 SKRHQKFTFLPRPDPVPERVPELYKDLLMYT 211
DB 181 SKRHQKFTFLPRPDPVPERVPELYKDLLMYT 211

RESULT 5
AAB62817
ID AAB62817 standard; Protein; 211 AA.
XX
AC AAB62817;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human fibroblast growth factor-CX (FGF-CX) amino acid sequence.
XX
KW Fibroblast growth factor-CX; FGF-CX; wound healing; haematopoiesis;
KW cell growth; proliferation; tumour; restenosis; psoriasis; human;
KW Dupuytren's contracture; Kaposi sarcoma; rheumatoid arthritis;
KW cartilage repair; bone repair; exostosis; hallux valgus deformity;
KW achondroplasia; cerebral lesion; cerebral oedema; senile dementia;
KW Alzheimer's disease; diabetic neuropathy; osteoporosis.
XX
OS Homo sapiens.
XX
PN WO200107595-A2.
XX
PD 01-FEB-2001.
XX
PF 27-JUL-2000; 2000WO-US20405.
XX
PR 27-JUL-1999; 99US-0145899.
PR 31-JAN-2000; 2000US-0494585.
PR 03-JUL-2000; 2000US-0609543.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Jeffers M, Shimkets RA, Prayaga SK, Boldog FL, Yang M, Burgess C;
PI Fernandes E, Herrmann JL, Larochele WJ, Lichenstein H;
XX
DR WPI; 2001-159717/16.
DR N-PSDB; AAF62049.
XX
PT New human fibroblast growth factor FGF-CX polypeptide, useful for
PT treating tissue proliferation disorders such as tumors, restenosis,
PT psoriasis, diabetic complications, Kaposi sarcoma and rheumatoid
PT arthritis -
XX
PS Claim 1; Fig 1; 128pp; English.
XX
CC This invention relates to human fibroblast growth factor-CX (FGF-CX) and
CC the DNA sequence encoding it. FGF-CX protein and polynucleotide sequences
CC are useful for treating or preventing a disorder associated with aberrant
CC expression, processing or physiological interactions of FGF-CX
CC characterised by insufficient or ineffective growth of a cell or tissue.
CC FGF-CX is also useful for promoting growth of cells which are in the
CC vicinity of a wound, vascular system, those involved in haematopoiesis or
CC erythropoiesis, cells in the lining of the gastrointestinal tract or
CC cells in hair follicles. Other uses include, inhibiting cell growth.
CC FGF-CX is useful for treating, preventing or delaying a tissue
CC proliferative disorder such as tumours, restenosis, psoriasis,
CC Dupuytren's contracture, diabetic complications, Kaposi sarcoma, and
CC rheumatoid arthritis. Compositions containing FGF-CX can be used to
CC stimulate cartilage or bone repair. Compositions containing FGF-CX
CC binding agents can be used to treat diseases such as multiple or solitary
CC hereditary exostosis, hallux valgus deformity and achondroplasia. FGF-CX
CC may be used in diagnosing or treating glial cell related disorders,
CC cerebral lesions or to treat cerebral oedema, senile dementia,
CC Alzheimer's disease, or diabetic neuropathy. FGF-CX also has
CC osteogenesis-promoting activity and can be used for treating bone
CC fractures and osteoporosis. FGF-CX polypeptides may be used as platelet
CC increasing agents, or for treating cerebral nervous diseases. The present
CC sequence represents the human FGF-CX protein.
XX
SQ Sequence 211 AA;

Query Match 100.0%; Score 1118; DB 22; Length 211;

Best Local Similarity 100.0%; Pred. No. 2.9e-111;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPLAEVGGFLGGLGEGQGVGSHFLPPAGERPPILLGERRSAAERSARGGPGCAOIAHL 60
DB 1 MAPLAEVGGFLGGLGEGQGVGSHFLPPAGERPPILLGERRSAAERSARGGPGCAOIAHL 60
QY 61 HGILRRRLQYCRTHLQILPDGVSQGTRODHSILFGILEFISVAVGLSVIRGVDGLYL 120
DB 61 HGILRRRLQYCRTHLQILPDGVSQGTRODHSILFGILEFISVAVGLSVIRGVDGLYL 120
QY 121 MNDKGYLGSEKLTSECIFREQEENWYNTYSSNIYKHGDTGRYFVALNKDGTPRDGR 180
DB 121 MNDKGYLGSEKLTSECIFREQEENWYNTYSSNIYKHGDTGRYFVALNKDGTPRDGR 180
QY 181 SKRHQKTHFLPRVDPDPVPELYKDLMLMT 211
DB 181 SKRHQKTHFLPRVDPDPVPELYKDLMLMT 211
RESULT 6
AAU02080
ID AAU02080 standard; Protein; 212 AA.
XX
AC AAU02080;
XX
DT 07-SEP-2001 (first entry)
XX
DE Rat fibroblast growth factor 20, FGF-20.
XX
KW Rat; fibroblast growth factor 20; FGF-20; Parkinson's disease;
KW substantia nigra; dopaminergic neuron; cochlea-associated disease;
KW otosclerosis; Cogan's syndrome; Meniere's disease; Pendred's syndrome;
KW diabetes-associated hearing loss; congenital malformations;
KW autoimmune disease-related hearing loss; age-related hearing loss;
KW deafness; ischaemia-related hearing disturbance; immunogen;
KW antibody; neuro-degenerative disease; tendonitis; wound healing;
KW stroke; ischaemia.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT Peptide 56..70
FT /label= Epitope
FT /note= "Peptide used to raise anti-FGF-20 antibodies"
FT Binding-site 170..186
FT /label= Heparin_binding_site
FT Peptide 176..189
FT /label= Epitope
FT /note= "Peptide used to raise anti-FGF-20 antibodies"
XX
PN WO200131008-A2.
XX
PD 03-MAY-2001.
XX
PF 20-OCT-2000; 2000WO-US29237.
XX
PR 22-OCT-1999; 99US-0161162.
PR 08-MAR-2000; 2000US-0187856.
XX
PA (CHIR) CHIRON CORP.
PA (KYOU) UNIV KYOTO.
XX
PI Itoh N, Kavanaugh WM;
XX
DR WPI; 2001-308642/32.
DR N-PSDB; AAS03276.
XX
PT New human and rat Fibroblast Growth Factor (FGF) polypeptides for
PT providing trophic support for cells used in Parkinson patients, and
PT alleviating brain and cochlea conditions -
XX
PS Claim 45; Fig 7; 73pp; English.

XX The sequence is Rat fibroblast growth factor 20, FGF-20. The FGF
 CC polypeptides and nucleic acids encoding them are useful for providing
 CC trophic support for cells in a patient, especially a patient with
 CC Parkinson's disease, and FGF-20 is additionally used to treat patients
 CC with conditions of the substantia nigra. The polypeptides and nucleic
 CC acids are useful for alleviating human brain conditions by slowing
 CC degeneration, restoring function of, or increasing the number of,
 CC dopaminergic neurons. The polypeptides and nucleic acids are also
 CC useful for alleviating cochlea-associated disease by slowing
 CC degeneration of or restoring or maintaining normal function of the
 CC structure of cochlea, where the disease is otosclerosis, Cogan's
 CC syndrome, Meniere's disease, Pendred's syndrome, diabetes-associated
 CC hearing loss, congenital malformations, autoimmune disease-related
 CC of FGF receptor and ischaemia-related hearing disturbance. Other
 CC diseases thought to be amenable to FGF therapeutic activity include
 CC neuro-degenerative diseases, tendonitis, wound healing, stroke and
 CC ischaemia. The polypeptides can be used to screen for agonists and
 CC antagonists. Epitope bearing fragments of the FGF-20 polypeptides can be
 CC used to raise anti-FGF-20 antibodies.

XX Sequence 212 AA;

Query Match 96.1%; Score 1074; DB 22; Length 212;
 Best Local Similarity 95.3%; Pred. No. 1.5e-106;
 Matches 201; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAPLAEVGGFLGLEIGQVQSGHFLPPAGERPPLLGERRSAERSARGGPGCAQLAHL 60
 DB 1 MAPTEVGAFLGLEIGQVQSGHFLPPAGERPPLLGERRGALERAGGPGSVELAHL 60
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 DB 61 HGILRRQLXCRTGFHLQILPDGVSQGTQDHSFLGILEFISVAVGLVSIRGVDGLYIG 120
 QY 121 MNDKGLYSGEKLTSCEIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTFRDGR 180
 DB 121 MNGKGLYSGEKLTSCEIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTFRDGR 180
 QY 181 SKRHQKTFHFLPRVDPERPVELYKDLLMT 211
 DB 181 SKRHQKTFHFLPRVDPERPVELYKDLLVYT 211

RESULT 7

AAW11548
 ID AAW11548 standard; Protein; 220 AA.

XX AAW11548;

DT 17-SEP-1997 (first entry)

DE Amino acid sequence of chicken FGF9 encoded by FGF9:pET-3C.

XX Mouse; chicken; fibroblast growth factor 9; FGF9; detection;
 KW fibroblast growth factor receptor 3; FGF9; cartilage repair;
 KW bone repair; antagonist; anti-FGF9 antibody; endochondromas;
 KW solitary hereditary exostosis; multiple hereditary exostosis;
 KW hallux valgus deformity; achondroplasia; synovial chondromatosis.

XX Gallus domesticus.

XX Key Location/Qualifiers

FH Misc-difference 216

FT /note= "Given in the specification as J, encoded by TGA"

XX WO9641523-A1.

XX 27-DEC-1996.

XX 12-JUN-1996; 96WO-IL00011.

XX

PR 12-JUN-1995; 95US-0000137.
 XX (YEDA) YEDA RES & DEV CO LTD.
 PA Yapon A;
 XX WP1: 1997-065215/06.
 DR N-PSDB; AAT58531.
 XX Medical and diagnostic use of fibroblast growth factor 9 - and
 PT recombinant fibroblast growth factor 9 DNA
 PS Claim 13; Fig 2; 32pp; English.

XX The sequences given in RAW11547-48 represent mouse and chicken
 CC fibroblast growth factor 9 (FGF9) respectively. FGF9 may be used in the
 CC method of the invention for detecting fibroblast growth factor receptor 3
 CC (FGFR3) in a sample or tissue. The method comprises contacting the
 CC sample or tissue with FGF9, allowing formation of receptor-ligand pairs,
 CC and detecting any FGFR3-FGF9 pairs. Compositions containing FGF9 can
 CC be used to increase FGFR3 activity, esp. to stimulate cartilage or bone
 CC repair. Compositions containing FGF9 antagonists or FGF9 binding agents
 CC (e.g. anti-FGF9 antibodies) can be used to treat diseases caused by an
 CC excess of FGF9 or overactivity of FGFR3, esp. multiple or solitary
 CC hereditary exostosis, hallux valgus deformity, achondroplasia, synovial
 CC chondromatosis and endochondromas.

XX Sequence 220 AA;

Query Match 69.6%; Score 778.5; DB 18; Length 220;
 Best Local Similarity 71.6%; Pred. No. 5.8e-75;
 Matches 151; Conservative 19; Mismatches 32; Indels 9; Gaps 4;

QY 1 MAPLAEVGGFLGLEIGQVQSGHFLPPAGERPPLLGERRSAERSARG---GPGAAQL 57
 DB 8 MAPLGEVGVYQDAV--PFGNVNPAIP--ADSPVLLSDHLGQAE--AGGLPRGAVYDL 61
 QY 58 AHLHGLIRRLQXCRTGFHLQILPDGVSQGTQDHSFLGILEFISVAVGLVSIRGVDGL 117
 DB 62 DHUKGILIRRLQXCRTGFHLQILPDGVSQGTQDHSFLGILEFISVAVGLVSIRGVDGL 121
 QY 118 YLGMNDKGLYSGEKLTSCEIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTFRD 177
 DB 122 YLGMNKGELYSGEKLTSCEIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTFRD 177
 QY 178 GAKSRHQKTFHFLPRVDPERPVELYKDLL 208
 DB 182 GTRTKRHQKTFHFSRPRVDPKVPVELYKDLL 212

RESULT 8

AAR27207
 ID AAR27207 standard; Protein; 208 AA.

XX AAR27207;

DT 20-MAY-1998 (first entry)

XX Glia activating factor #1.

XX GAF; stimulates glial cell growth; cerebral nerve cell lesions;
 KW cerebral oedema; alzheimers disease; senile dementia;
 KW diabetic neuropathy; stimulates fibroblasts; burns; wounds; ulcers;
 KW stimulates megakaryocytes; increase platelets; haematopoietic cells;
 KW immunocompetent cells; vascular smooth muscle cells; bone fractures;
 KW osteogenesis promoting activity; osteoporosis; cerebral tumours;
 KW stimulates cultured cells.

XX Homo sapiens.

XX EP503297-A.

XX 16-SEP-1992.

XX

```

XX PF 13-FEB-1992; 92EP-0102385.
XX OS Homo sapiens.
XX PN EP503297-A.
XX PD 16-SEP-1992.
XX PF 13-FEB-1992; 92EP-0102385.
XX PR 14-FEB-1991; 91JP-0020860.
XX PR 04-SEP-1991; 91JP-0224454.
XX PR 10-JAN-1992; 92JP-0003399.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX PI Kondo T, Kurokawa T, Naruo K, Seko C;
XX DR WPI; 1992-309482/38.
XX DR WPI; 1992-309482/38.
XX PT Glia activating factor and its DNA - specifically promotes growth
XX of glial cells, for treating e.g. cerebral lesions, Alzheimer's
XX disease, diabetic neuropathies, etc., also in diagnosis
XX PS Claim 1; Pg5; 7pp; English.
XX CC This sequence represents a glia activating factor. It stimulates the
XX growth of glia cells and can be used to accelerate healing of cerebral
XX lesions or treat cerebral oedema, alzheimers disease, senile dementia,
XX or diabetic neuropathy. It also stimulates fibroblasts (to increase the
XX healing of burns, wounds, ulcers, etc) megakaryocytes (to increase the
XX no. of platelets), haematopoietic, immunocompetent and vascular smooth
XX muscle cells. It is also expected to have osteogenesis-promoting activity
XX (for treating bone fractures and osteoporosis) Assay of this factor may
XX be useful in diagnosis of cerebral tumours, and antibodies against could
XX be used to treat such tumours. It can also be used as a reagent for
XX stimulating growth of cultured cells. Dosage is lng-0.1mg/kg/day.
XX SQ Sequence 208 AA;

Query Match 69.3%; Score 774.5; DB 13; Length 208;
Best Local Similarity 70.6%; Pred. No. 1.5e-74;
Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;

QY 1 MAPLAEVGGFGLGGLGQQVGSFLLPPAGERPPLGERRSAAERSARG---GPGAAOL 57
DB 1 MAPLGEVGNVGVQDAV--PFGNVPLPV--DSPVLLSDHLGQSE--AGGLPRGPVATDL 54
QY 58 AHLHGILRRRLQYCRTHLQILPDGVSQGTRODHSFLGILEFISVAVGLVSRGVDSGL 117
DB 55 DHLKGILRRRLQYCRTHLQILPDGVSQGTRODHSFLGILEFISVAVGLVSRGVDSGL 114
QY 118 YLGMNDKGLYGSSEKLTSECFRQFENWNTYSSNLYKHVDTGRRYFVALNKDGT 177
DB 115 YLGMNEKGLYGSSEKLTQECVFRQFENWNTYSSNLYKHVDTGRRYFVALNKDGT 174
QY 178 GARSRRHOKHFTFLPRPVDPERVPPELYKDLL 208
DB 175 GTRTKRHOKHFTFLPRPVDPERVPPELYKDLL 205

RESULT 10
AAR56505
ID AAR56505 standard; peptide; 208 AA.
XX AC AAR56505;
XX DT 06-MAR-1995 (first entry)
XX DE Glia activating factor (GAF) peptide.
XX KW Glia activating factor; GAF; testing; detection; antibody; cancer;
XX osteogenesis; platelet; hepatopathy; cirrhosis; anticancer agent.
XX

XX PF 13-FEB-1992; 92EP-0102385.
XX OS Homo sapiens.
XX PN EP503297-A.
XX PD 16-SEP-1992.
XX PF 13-FEB-1992; 92EP-0102385.
XX PR 14-FEB-1991; 91JP-0020860.
XX PR 04-SEP-1991; 91JP-0224454.
XX PR 10-JAN-1992; 92JP-0003399.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX PI Kondo T, Kurokawa T, Naruo K, Seko C;
XX DR WPI; 1992-309482/38.
XX DR WPI; 1992-309482/38.
XX PT Glia activating factor and its DNA - specifically promotes growth
XX of glial cells, for treating e.g. cerebral lesions, Alzheimer's
XX disease, diabetic neuropathies, etc., also in diagnosis
XX PS Claim 1; Fig 19; 87pp; English.
XX CC This sequence represents a glia activating factor. It is expressed
XX in monkey COS-7 cells. It stimulates the growth of glia cells and
XX can be used to accelerate healing of cerebral lesions or treat cerebral
XX oedema, alzheimers disease, senile dementia, or diabetic neuropathy. It
XX also stimulates fibroblasts (for accelerating healing of burns, wounds,
XX ulcers, etc) megakaryocytes (to increase the no. of platelets),
XX haematopoietic, immunocompetent and vascular smooth muscle cells. It is
XX also expected to have osteogenesis-promoting activity (for treating
XX bone fractures and osteoporosis) Assay of this factor may be useful in
XX diagnosis of cerebral tumours, and antibodies against could be used to
XX treat such tumours. It can also be used as a reagent for stimulating
XX growth of cultured cells. Dosage is lng-0.1mg/kg/day.
XX SQ Sequence 208 AA;

Query Match 69.3%; Score 774.5; DB 13; Length 208;
Best Local Similarity 70.6%; Pred. No. 1.5e-74;
Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;

QY 1 MAPLAEVGGFGLGGLGQQVGSFLLPPAGERPPLGERRSAAERSARG---GPGAAOL 57
DB 1 MAPLGEVGNVGVQDAV--PFGNVPLPV--DSPVLLSDHLGQSE--AGGLPRGPVATDL 54
QY 58 AHLHGILRRRLQYCRTHLQILPDGVSQGTRODHSFLGILEFISVAVGLVSRGVDSGL 117
DB 55 DHLKGILRRRLQYCRTHLQILPDGVSQGTRODHSFLGILEFISVAVGLVSRGVDSGL 114
QY 118 YLGMNDKGLYGSSEKLTSECFRQFENWNTYSSNLYKHVDTGRRYFVALNKDGT 177
DB 115 YLGMNEKGLYGSSEKLTQECVFRQFENWNTYSSNLYKHVDTGRRYFVALNKDGT 174
QY 178 GARSRRHOKHFTFLPRPVDPERVPPELYKDLL 208
DB 175 GTRTKRHOKHFTFLPRPVDPERVPPELYKDLL 205

RESULT 9
AAR27213
ID AAR27213 standard; Protein; 208 AA.
XX AC AAR27213;
XX DT 20-MAY-1998 (first entry)
XX DE Glia activating factor #7.
XX KW GAF; stimulates glial cell growth; cerebral nerve cell lesions;
XX cerebral oedema; alzheimers disease; senile dementia;
XX diabetic neuropathy; stimulates fibroblasts; burns; wounds; ulcers;
XX stimulates megakaryocytes; increase platelets; haematopoietic cells;
XX immunocompetent cells; vascular smooth muscle cells; bone fractures;
XX osteogenesis promoting activity; osteoporosis; cerebral tumours;
XX stimulates cultured cells.

```


KW FGF-9; fibroblast growth factor; cytotoxic conjugate; fusion protein;
 KW saporin; cytostatic; tumor; diabetes; rheumatoid arthritis.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 68
 FT /note- "Cys may be replaced by Ser"
 XX
 XX W09503831-A.
 XX
 XX 09-FEB-1995.
 XX
 XX 27-JUL-1994; 94WO-US08511.
 XX
 XX 02-AUG-1993; 93US-0099924.
 XX 29-OCT-1993; 93US-0145829.
 XX
 XX (PRIZ-) PRIZM PHARM INC.
 XX (WHIT-) WHITTIER INST DIABETES & ENDOCRINOLOGY.
 XX
 XX Baird AJ, Lappi DA, Sosnowski BA;
 XX WPI; 1995-082038/11.
 XX
 XX New monogenous preparations of cytotoxic conjugates and DNA -
 XX contain fibroblast growth factors and cytotoxic agents for
 XX treating FGF conditions such as tumours, diabetes and rheumatoid
 XX arthritis.
 XX
 XX Disclosure; Page 115-116; 128pp; English.
 XX
 XX Novel fusion proteins comprise FGF linked to saporin. FGF-1 to -9
 XX may be used, pref. mutants in which at least 1 Cys residue is
 XX replaced by conservative Ser substitutions. The fusion proteins
 XX are potent cytotoxic agents to cells bearing the FGF receptor.
 XX
 XX Sequence 208 AA;
 SQ
 Query Match 69.3%; Score 774.5; DB 16; Length 208;
 Best Local Similarity 70.6%; Pred. No. 1.5e-74;
 Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;
 QY 1 MAPLAEEVGGFLGGLGQVGSFHLPPAGERPPLLGERRSAAERSARG---GPGAAQL 57
 DB 1 MAPLGEVNTFGVQDAV--PFGNVPVLPV--DSPVLLSDHLGQSE--AGGLPRGPAVTDL 54
 QY 58 AHLHGILRRRLQYCRGTGFHLQILPDGVSQGTRODHSFLGILEFISVAVGLVSIRGVDSGL 117
 DB 55 DHLKGILRRRLQYCRGTGFHLEIFPNGTIQTRKDHRSRFGILEFISIAVGLVSIRGVDSGL 114
 QY 118 YLGMNDKGLYSGEKLISECIRFQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPTD 177
 DB 115 YLGMNEKGLYSGEKLITQECVFRQFEENWNTYSSNLYKHVDTRRRYFVALNKDGTPTRE 174
 QY 178 GASKRKHQKFTFLPRPVDPRVPELYKDIL 208
 DB 175 GTRTKRKHQKFTFLPRPVDPKVPELYKDIL 205
 RESULT 13
 ID AAW11547
 XX AAW11547 standard; Protein; 208 AA.
 XX
 XX AAW11547;
 XX
 XX 17-SEP-1997 (first entry)
 XX
 XX Amino acid sequence of mouse FGF9 encoded by FGF9:pET-3C.
 XX
 XX Mouse; chicken; fibroblast growth factor 9; FGF9; detection;
 XX fibroblast growth factor receptor 3; FGFR3; cartilage repair;
 KW bone repair; antagonist; anti-FGF9 antibody; endochondromas;
 KW

KW solitary hereditary exostosis; multiple hereditary exostosis;
 KW hallux valgus deformity; achondroplasia; synovial chondromatosis.
 XX Mus musculus.
 OS
 XX
 PN W09641523-A1.
 XX
 XX 27-DEC-1996.
 PD
 XX 12-JUN-1996; 96WO-IL00011.
 XX
 XX 12-JUN-1995; 95US-0000137.
 PR
 XX (YEDA) YEDA RES & DEV CO LTD.
 PA
 XX Yayon A;
 PI
 XX WPI; 1997-065215/06.
 XX N-PSDB; AAT58530.
 DR
 XX Medical and diagnostic use of fibroblast growth factor 9 - and
 XX recombinant fibroblast growth factor 9 DNA
 PT
 XX Claim 12; Fig 1; 32pp; English.
 PS
 XX The sequences given in AAW11547-48 represent mouse and chicken
 XX fibroblast growth factor 9 (FGF9), respectively. FGF9 may be used in the
 XX method of the invention for detecting fibroblast growth factor receptor 3
 XX (FGFR3) in a sample or tissue. The method comprises contacting the
 XX sample or tissue with FGF9, allowing formation of receptor-ligand pairs,
 XX and detecting any FGFR3-FGF9 pairs. Compositions containing FGF9 can
 XX be used to increase FGFR3 activity, esp. to stimulate cartilage or bone
 XX repair. Compositions containing FGF9 antagonists or FGF9 binding agents
 XX (e.g. anti-FGF9 antibodies) can be used to treat diseases caused by an
 XX excess of FGF9 or overactivity of FGFR3, esp. multiple or solitary
 XX hereditary exostosis, hallux valgus deformity, achondroplasia, synovial
 XX chondromatosis and endochondromas.
 XX
 XX Sequence 208 AA;
 SQ
 Query Match 69.3%; Score 774.5; DB 18; Length 208;
 Best Local Similarity 70.6%; Pred. No. 1.5e-74;
 Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;
 QY 1 MAPLAEEVGGFLGGLGQVGSFHLPPAGERPPLLGERRSAAERSARG---GPGAAQL 57
 DB 1 MAPLGEVNTFGVQDAV--PFGNVPVLPV--DSPVLLSDHLGQSE--AGGLPRGPAVTDL 54
 QY 58 AHLHGILRRRLQYCRGTGFHLQILPDGVSQGTRODHSFLGILEFISVAVGLVSIRGVDSGL 117
 DB 55 DHLKGILRRRLQYCRGTGFHLEIFPNGTIQTRKDHRSRFGILEFISIAVGLVSIRGVDSGL 114
 QY 118 YLGMNDKGLYSGEKLISECIRFQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPTD 177
 DB 115 YLGMNEKGLYSGEKLITQECVFRQFEENWNTYSSNLYKHVDTRRRYFVALNKDGTPTRE 174
 QY 178 GASKRKHQKFTFLPRPVDPRVPELYKDIL 208
 DB 175 GTRTKRKHQKFTFLPRPVDPKVPELYKDIL 205
 RESULT 14
 ID AAW75719
 XX AAW75719 standard; Protein; 208 AA.
 XX
 XX AAW75719;
 XX
 XX 07-DEC-1998 (first entry)
 XX
 XX Fibroblast growth factor-9.
 XX Fibroblast growth factor-9; FGF-9; mutein; protein engineering;
 KW heparin; thrombosis; thrombocytopenia; ophthalmic disorder;
 KW

Db 175 GTRTKRHQKFTHELPRPVDKVPKLYKDIL 205

Search completed: October 21, 2002, 16:14:15
Job time : 33 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 21, 2002, 16:13:40 ; Search time 13 Seconds
(without alignments)
396.446 Million cell updates/sec

Title: US-09-817-814-2

Perfect score: 1118

Sequence: 1 MAPLAEVGGFLGGLGQQ.....PRPVDPERVPELYKDLLMYT 211

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

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4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*

5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*

6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	774.5	69.3	208	1	US-08-340-820-3
2	774.5	69.3	208	1	US-08-340-820-9
3	774.5	69.3	208	1	US-08-340-820-25
4	774.5	69.3	208	1	US-08-172-328-3
5	774.5	69.3	208	1	US-08-593-535-3
6	774.5	69.3	208	1	US-08-593-535-9
7	774.5	69.3	208	1	US-08-593-535-25
8	774.5	69.3	208	1	US-08-439-725A-7
9	774.5	69.3	208	1	US-08-462-169B-17
10	774.5	69.3	208	2	US-08-207-412B-13
11	774.5	69.3	208	2	US-08-867-471-7
12	774.5	69.3	208	2	US-08-438-439C-12
13	774.5	69.3	208	2	US-08-951-822-34
14	774.5	69.3	208	2	US-08-943-915-3
15	774.5	69.3	208	3	US-09-103-079-17
16	774.5	69.3	208	3	US-08-705-245-7
17	774.5	69.3	208	3	US-08-718-904-18
18	774.5	69.3	208	3	US-09-023-082A-18
19	774.5	69.3	208	4	US-09-368-951-34
20	769.5	68.8	207	1	US-08-340-820-2
21	769.5	68.8	207	1	US-08-172-328-2
22	769.5	68.8	207	1	US-08-593-535-2
23	769.5	68.8	208	1	US-08-464-590A-10
24	769.5	68.8	208	3	US-09-093-585-10
25	769.5	68.8	205	1	US-08-340-820-5
26	758.5	67.8	205	1	US-08-172-328-4
27	758.5	67.8	205	1	US-08-593-535-5

28	758.5	67.8	206	1	US-08-340-820-7	Sequence 7, Appli
29	758.5	67.8	206	1	US-08-340-820-8	Sequence 8, Appli
30	758.5	67.8	206	1	US-08-172-328-5	Sequence 5, Appli
31	758.5	67.8	206	1	US-08-593-535-7	Sequence 7, Appli
32	758.5	67.8	206	1	US-08-593-535-8	Sequence 8, Appli
33	742	66.4	175	1	US-08-172-328-6	Sequence 6, Appli
34	742	66.4	176	1	US-08-172-328-7	Sequence 7, Appli
35	742	66.4	177	1	US-08-340-820-4	Sequence 4, Appli
36	742	66.4	177	1	US-08-593-535-4	Sequence 4, Appli
37	742	66.4	178	1	US-08-340-820-6	Sequence 6, Appli
38	742	66.4	178	1	US-08-593-535-6	Sequence 6, Appli
39	729	65.2	159	1	US-08-172-328-8	Sequence 8, Appli
40	729	65.2	160	1	US-08-172-328-9	Sequence 9, Appli
41	710.5	63.6	193	2	US-08-438-439C-21	Sequence 21, Appli
42	708.5	63.4	207	2	US-08-943-915-5	Sequence 5, Appli
43	705.5	63.1	207	2	US-08-943-915-2	Sequence 2, Appli
44	702.5	62.8	190	1	US-08-441-629-16	Sequence 16, Appli
45	702.5	62.8	190	3	US-08-776-207-16	Sequence 16, Appli

ALIGNMENTS

RESULT 1
US-08-340-820-3
; Sequence 3, Application US/08340820
; Patent No. 5512460
; GENERAL INFORMATION:
; APPLICANT: NARUO, Ken-ichi
; APPLICANT: SEKO, Chisako
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KONDO, Tatsuya
; TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND ITS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,820
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/835,713
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G.
; REGISTRATION NUMBER: 27026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-340-820-3

Query Match 69.3%; Score 774.5; DB 1; Length 208;
Best Local Similarity 70.6%; Pred. No. 2e-79;
Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;


```
QY 1 MAPLAEVGFLGGLGQQVGSFHLPPAGERPPLLGERSSAERSARG---GPGAAQL 57
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Db 1 MAPLGEVGNVGVQDAV--PFGNVPVLPV--DSPVLLSDHLGQSE--AGGLPRGPAVTDL 54

QY 58 AHLHGILRRRLQYCRTHLQILPDGSGVQGTRODHSFLGILEFISVAVGLSVIRGVDSGL 117
||||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 55 DHLKGLRRRLQYCRTHLQILPDGSGVQGTRODHSFLGILEFISVAVGLSVIRGVDSGL 114

QY 118 YLGMNDKGLYSGKLTSECFRQFEENWNTYSSNIYKHGDTGRYFVALNKDGTPRD 177
||||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 115 YLGMNEKGLYSGKLTQECVFRQFEENWNTYSSNLYKHVDTRGRYYVALNKDGTPE 174

QY 178 GARSKRHOKETHFLPRPDPVPERVPELYKDIL 208
| : ||||| : : : : : : : : : : : : : : : : : : : : : :
Db 175 GTRTKRHOKETHFLPRPDPVDPKVPELYKDIL 205
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RESULT 4

```
US-08-172-328-3
; Sequence 3, Application US/08172328
; Patent No. 5571895
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KUROHIMA, Ken-ichi
; APPLICANT: YOSHITOMI, Sumie
; APPLICANT: SEKO, Sachiko
; TITLE OF INVENTION: ANTIODIES, POLYPEPTIDES, PRODUCTION AND
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/172,328
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: NEUNER, George W
; REGISTRATION NUMBER: 26964
; REFERENCE/DOCKET NUMBER: 26964
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; HAPLOTYPE: 2n
; TISSUE TYPE: Skin
; CELL TYPE: Fibroblast
; IMMEDIATE SOURCE:
; LIBRARY: Human foreskin cDNA library
; CLONE: pGAF1
US-08-172-328-3
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Query Match 69.3%; Score 774.5; DB 1; Length 208;
Best Local Similarity 70.6%; Pred. No. 2e-79;

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Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;
QY 1 MAPLAEVGFLGGLGQQVGSFHLPPAGERPPLLGERSSAERSARG---GPGAAQL 57
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Db 1 MAPLGEVGNVGVQDAV--PFGNVPVLPV--DSPVLLSDHLGQSE--AGGLPRGPAVTDL 54

QY 58 AHLHGILRRRLQYCRTHLQILPDGSGVQGTRODHSFLGILEFISVAVGLSVIRGVDSGL 117
||||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 55 DHLKGLRRRLQYCRTHLQILPDGSGVQGTRODHSFLGILEFISVAVGLSVIRGVDSGL 114

QY 118 YLGMNDKGLYSGKLTSECFRQFEENWNTYSSNIYKHGDTGRYFVALNKDGTPRD 177
||||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 115 YLGMNEKGLYSGKLTQECVFRQFEENWNTYSSNLYKHVDTRGRYYVALNKDGTPE 174

QY 178 GARSKRHOKETHFLPRPDPVPERVPELYKDIL 208
| : ||||| : : : : : : : : : : : : : : : : : : : : : :
Db 175 GTRTKRHOKETHFLPRPDPVDPKVPELYKDIL 205
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RESULT 5

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US-08-593-535-3
; Sequence 3, Application US/08593535
; Patent No. 562928
; GENERAL INFORMATION:
; APPLICANT: NARUO, Ken-ichi
; APPLICANT: SEKO, Chisako
; APPLICANT: KURAKAWA, Tsutomu
; APPLICANT: KONDO, Tatsuya
; TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND ITS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/593,535
; FILING DATE: 24-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/835,713
; FILING DATE: 12-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G.
; REGISTRATION NUMBER: 27026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-593-535-3
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Query Match 69.3%; Score 774.5; DB 1; Length 208;
Best Local Similarity 70.6%; Pred. No. 2e-79;
Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;

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QY 1 MAPLAEVGFLGGLGQQVGSFHLPPAGERPPLLGERSSAERSARG---GPGAAQL 57
||||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MAPLGEVGNVGVQDAV--PFGNVPVLPV--DSPVLLSDHLGQSE--AGGLPRGPAVTDL 54
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Qy 58 AHLHGILRRRLQYCRGTGFHLLQILPDGSGVQCTRODHSIFGLILEFTISVAGLVSIIRGVDSGL 117
|| |||||RRRLQYCRGTGFHLLQILPDGSGVQCTRODHSIFGLILEFTISVAGLVSIIRGVDSGL 114
Db 55 DHLAKGILRRRLQYCRGTGFHLLQILPDGSGVQCTRODHSIFGLILEFTISVAGLVSIIRGVDSGL 114
Qy 118 YLGMNDKGLYSEKLTSECIFREQFEENWYNTYSSNLYKHGDTGRRYFVALNKDGTTPR 177
|||||RRRLQYCRGTGFHLLQILPDGSGVQCTRODHSIFGLILEFTISVAGLVSIIRGVDSGL 174
Db 115 YLGMNEKGLYSEKLTSECIFREQFEENWYNTYSSNLYKHGDTGRRYFVALNKDGTTPRE 174
Qy 178 GARSKRHQKFTFLPRPDPKVPPELYKDIL 208
| | |||||RRRLQYCRGTGFHLLQILPDGSGVQCTRODHSIFGLILEFTISVAGLVSIIRGVDSGL 205
Db 175 GTRTKRHKQKFTFLPRPDPKVPPELYKDIL 205

RESULT 6
US-08-593-535-9
; Sequence 9, Application US/08593535
; Patent No. 5622928
; GENERAL INFORMATION:
; APPLICANT: NARUO, Ken-ichi
; APPLICANT: SEKO, Chisako
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KONDO, Tatsuya
; TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND ITS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/593,535
; FILING DATE: 24-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/835,713
; FILING DATE: 12-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G.
; REGISTRATION NUMBER: 27026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-593-535-9

Query Match 69.3%; Score 774.5; DB 1; Length 208;
Best Local Similarity 70.6%; Pred. No. 2e-79;
Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;
Qy 1 MAPLAEVGFLGLEGQQVGSFLLPPAGERPPLLGERRSAAERSARG---GPGAAQL 57
Db 1 MAPLGEVGNVFGQDAV--PFGNVPVLPV--DSPVLLSDHLGQSE--AGGLPRGPVAVTDL 54
Qy 58 AHLHGILRRRLQYCRGTGFHLLQILPDGSGVQCTRODHSIFGLILEFTISVAGLVSIIRGVDSGL 117
Db 55 DHLAKGILRRRLQYCRGTGFHLLQILPDGSGVQCTRODHSIFGLILEFTISVAGLVSIIRGVDSGL 114

Qy 118 YLGMNDKGLYSEKLTSECIFREQFEENWYNTYSSNLYKHGDTGRRYFVALNKDGTTPR 177
|||||RRRLQYCRGTGFHLLQILPDGSGVQCTRODHSIFGLILEFTISVAGLVSIIRGVDSGL 174
Db 115 YLGMNEKGLYSEKLTSECIFREQFEENWYNTYSSNLYKHGDTGRRYFVALNKDGTTPRE 174
Qy 178 GARSKRHQKFTFLPRPDPKVPPELYKDIL 208
| | |||||RRRLQYCRGTGFHLLQILPDGSGVQCTRODHSIFGLILEFTISVAGLVSIIRGVDSGL 205
Db 175 GTRTKRHKQKFTFLPRPDPKVPPELYKDIL 205

RESULT 7
US-08-593-535-25
; Sequence 25, Application US/08593535
; Patent No. 5622928
; GENERAL INFORMATION:
; APPLICANT: NARUO, Ken-ichi
; APPLICANT: SEKO, Chisako
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KONDO, Tatsuya
; TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND ITS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/593,535
; FILING DATE: 24-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/835,713
; FILING DATE: 12-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G.
; REGISTRATION NUMBER: 27026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; HAPLOTYPE: 2n
; TISSUE TYPE: skin
; CELL TYPE: fibroblast
; IMMEDIATE SOURCE:
; LIBRARY: Human foreskin cDNA library
; CLONE: pGAF1
; US-08-593-535-25

Query Match 69.3%; Score 774.5; DB 1; Length 208;
Best Local Similarity 70.6%; Pred. No. 2e-79;
Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;
Qy 1 MAPLAEVGFLGLEGQQVGSFLLPPAGERPPLLGERRSAAERSARG---GPGAAQL 57
Db 1 MAPLGEVGNVFGQDAV--PFGNVPVLPV--DSPVLLSDHLGQSE--AGGLPRGPVAVTDL 54

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Db      175  GTTRKRQKQKTHFLPREVDKDPKVELYKDIL 205
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```

CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESS: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,169B
FILING DATE: 05 JUN 95
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-441 (PF203)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1740
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-462-169B-17

Db	55	DHLKGLTLRRQDYCYGTGPHLEIFPNGTIQGTRKDHRSFGILEFISIAVLGLYSIRGVSGL	11
QY	118	YLGMDKGLYGESEKLTSECIFRQFQFENWNYTSSNIYKHGDTGRRYFVALNKDGT	177
Db	115	YLGMEKGLYGESEKLTQECVFRQFQFENWNYTSSNIYKHVDTCRRYFVALNKDGT	174
QY	178	GARSKRHQKETHFLPRPVDPRPVELYKDLL	208
Db	175	GTRKRHQKETHFLPRPVDPRPVELYKDL	205

RESULT 10
US-08-207-412B-13
: Sequence 13, Application US/08207412B
: Patent No. 5817485
: GENERAL INFORMATION:
: APPLICANT: Hu, Jing-Shan
: TITLE OF INVENTION: Fibroblast Growth Factor-10

QY	1	MAPLAEVGGFLGGLGQQVGS	HFLPPAGERPPULLGERRSAAERSARG---	GPGAQQL	57
Db	1	MAPLGEVNGYFCVQDAV--	PFGNVPVLPV--DSPVLLSDHLGQSE--	AGGLPRGPAYTDL	54
QY	58	AHLHGILRRRLCYCRTGFLHQL	PDGVSQCTRODHSFGILEFISVAVGLSVIRGDSGL		117

Db 175 GTRKRRHQKFTHFLPRVDPDKVPELYKDIL

Db 175 GTRTKRHQKFTHFLLPRPVDPKVPELYKDIL 205

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RESULT 15
US-09-103-079-17
; Sequence 17, Application US/09103079A
; Patent No. 6013477
; GENERAL INFORMATION:
; APPLICANT: Greene, John M.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Fibroblast Growth Factor 15
; FILE REFERENCE: PE203D1
; CURRENT APPLICATION NUMBER: US/09/103, 079A
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 08/462,169
; EARLIER FILING DATE: 1995-06-05
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-103-079-17

Query Match      69.3%; Score 774.5; DB 3; Length 208;
Best Local Similarity 70.6%; Pred. No. 2e-79;
Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;

QY 1 MAPLAEVGGFLGGLGQQVGSHELLPPAGERPPLLGERSSAERSARC---GPGAAQL 57
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Db 1 MAPLGEVGNRYGVQDAV--PFGNVPVLPV--DSPVLLSDHLGQSE--AGGLPRGPVTDL 54
   ||||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 58 AHLHGILRRRLQYCRGTFHQLIPDGSVQGTRODHSLEFISVAVGLVSIRGVDSGL 117
   ||||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 55 DHLKGILRRRLQYCRGTFHLEIFPFGTIQTRKDHRSREFILEFISIAVGLVSIRGVDSGL 114
   ||||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 118 YLGMNDKGELYGSEKLTSECFRQFENWNTYSSNIYKHGDTGRRYFVALNKDGTPRD 177
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Db 115 YLGMNEKGELYGSEKLTQECVFEQFENWNTYSSNLYKHVDTGRRYYVALNKDGTPRE 174
   ||||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 178 GARSRRHOKFTFLPRPVDPERVPPELYKDLL 208
   ||||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 175 GTTRKRHOKFTFLPRPVDPKVPPELYKDIL 205
   ||||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
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Search completed: October 21, 2002, 16:15:54
Job time : 14 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2002, 16:12:50 ; Search time 21 Seconds
(without alignments)
965.469 Million cell updates/sec

Title: US-09-817-814-2
Perfect score: 1118
Sequence: 1 MAPLAEVGGFLGGLEGLGQQ.....PRPVPDPVPELYKDLLMYT 211

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1118	100.0	211	2 JC7353	fibroblast growth
2	1074	96.1	212	2 JC7511	fibroblast growth
3	904.5	80.9	208	2 JC7082	fibroblast somatot
4	774.5	69.3	208	2 S66486	fibroblast growth
5	774.5	69.3	208	2 A48137	fibroblast growth
6	708.5	63.4	207	2 JC5941	fibroblast growth
7	705.5	63.1	207	2 JC5940	fibroblast growth
8	342.5	30.6	220	2 I50588	fibroblast growth
9	324.5	29.0	266	2 S68144	fibroblast growth
10	324	29.0	237	1 S39582	transforming prote
11	324	29.0	267	1 TVHUP5	fibroblast growth
12	321	28.7	264	2 A36207	fibroblast growth
13	319	28.5	239	1 S04742	fibroblast growth
14	317	28.4	245	1 TVMST2	transforming prote
15	307	27.5	256	2 JC4627	fibroblast growth
16	297	26.6	194	2 S26049	fibroblast growth
17	292	26.1	194	2 I48610	fibroblast growth
18	290	25.9	194	1 A36301	keratinocyte growt
19	290	25.9	194	2 S49501	fibroblast growth
20	289	25.8	168	2 JG0184	keratinocyte growt
21	288.5	25.8	194	2 I50710	fibroblast growth
22	282.5	25.3	208	2 S20102	fibroblast growth
23	281.5	25.2	208	2 S14192	fibroblast growth
24	279.5	25.0	187	2 S23595	embryonic fibrobla
25	278	24.9	413	2 H88481	protein let-756 [i
26	275	24.6	206	2 JC4268	fibroblast growth
27	270	24.2	206	1 TVHUNS	fibroblast growth
28	268.5	24.0	192	2 S54407	embryonic fibrobla
29	256	22.9	155	1 A60721	acidic fibroblast

30	256	22.9	202	1 TVMSHS	fibroblast growth
31	255	22.8	152	2 JH0476	acidic fibroblast
32	254.5	22.8	155	2 S04147	acidic fibroblast
33	254.5	22.8	155	2 D37360	acidic fibroblast
34	251	22.5	155	1 A33665	acidic fibroblast
35	243.5	21.8	155	2 A60130	acidic fibroblast
36	235.5	21.1	155	2 JW0055	acidic fibroblast
37	234.5	21.0	155	1 GKBOA	acidic fibroblast
38	218.5	19.5	210	2 A32398	basic fibroblast g
39	214	19.1	97	2 B46289	keratinocyte growt
40	213	19.1	98	2 C46289	keratinocyte growt
41	211.5	18.9	189	2 A48834	basic fibroblast g
42	209	18.7	157	1 GKBOB	basic fibroblast g
43	205	18.3	154	2 A31674	basic fibroblast g
44	204.5	18.3	154	2 C37360	basic fibroblast g
45	204.5	18.3	164	2 S31622	basic fibroblast g

ALIGNMENTS

RESULT 1
JC7353
fibroblast growth factor-20 - human
C:Species: Homo sapiens (man)
C:Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 01-Dec-2000
C:Accession: JC7353
R:Kirikoshi, H.; Sagara, N.; Saitoh, T.; Tanaka, K.; Sekihara, H.; Shlokawa, K.; Kato
Biochem. Biophys. Res. Commun. 274, 337-343, 2000
A:Title: Molecular cloning and characterization of human FGF-20 on chromosome 8p21.3-
A:Reference number: JC7353
A:Accession: JC7353
A:Molecule type: mRNA
A:Residues: 1-211 <KIR>
A:Cross-references: DDBJ:AB044277
C:Comment: This factor is involved in physiological and pathological processes, play
C:Genetics:
A:Gene: fgf-20
A:Map position: 8p21.3-8p22
C:Superfamily: fibroblast growth factor
C:Keywords: angiogenesis; carcinogenesis

Query Match	100.0%	Score 1118;	DB 2;	Length 211;
Best Local Similarity	100.0%;	Pred. No. 1.3e-97;		
Matches	211;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	
QY	1	MAPLAEVGGFLGGLEGLGQVGSFLLPPAGERPPLLGERRSAAERSARGGPGAAQLAHL	60	
Db	1	MAPLAEVGGFLGGLEGLGQVGSFLLPPAGERPPLLGERRSAAERSARGGPGAAQLAHL	60	
QY	61	HGILRRQLYCRGFGHLQILPDGVSQGTQDHSFLGILEFISVAVGLSVIRGVDSGLYL	120	
Db	61	HGILRRQLYCRGFGHLQILPDGVSQGTQDHSFLGILEFISVAVGLSVIRGVDSGLYL	120	
QY	121	MNDKGLYGESEKTSCEIFREQEENWNTYSSNIYKHGDTGRYFVALNKDGTTPRDGAR	180	
Db	121	MNDKGLYGESEKTSCEIFREQEENWNTYSSNIYKHGDTGRYFVALNKDGTTPRDGAR	180	
QY	181	SKRHQKTFHFLPRPDPDPVPELYKDLLMYT	211	
Db	181	SKRHQKTFHFLPRPDPDPVPELYKDLLMYT	211	

RESULT 2
JC7511
fibroblast growth factor-20 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: JC7511
R:Ohmachi, S.; Watanabe, Y.; Mikami, T.; Kusu, N.; Ibi, T.; Akaike, A.; Itoh, N.
Biochem. Biophys. Res. Commun. 277, 355-360, 2000
A:Title: FGF-20, a novel neurotrophic factor, preferentially expressed in the substan
A:Reference number: JC7511; MUID:20490008

```
A:Contents: Brain
A:Accession: JC7511
A:Molecule type: DNA
A:Residues: 1-212 <OHM>
A:Cross-references: DDBJ:AB020021
C:Comment: This factor is secreted, and plays an important role as a neurotrophic factor
C:Genetics:
A:Gene: fgf-20
C:Keywords: brain; growth factor; neurotrophic factor

Query Match      96.1%; Score 1074; DB 2; Length 212;
Best Local Similarity 95.3%; Pred. No. 1.7e-93;
Matches 201; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAPLAEVGGFLGGLGQVGSFLLPPAGERPPLLGERRSAAERSARGGPGAAQLAHL 60
DB 1 MAPLTVGAFLGGLGQVGSFLLPPAGERPPLLGERRGALRGARGGPGSVELAHL 60

QY 61 HGLRRRLQYCRGTGFHLQILPDGVSQGTRODHSFLGILEFISVAVGLVSRGVDSGLYL 120
DB 61 HGLRRRLQYCRGTGFHLQILPDGVSQGTRODHSFLGILEFISVAVGLVSRGVDSGLYL 120

QY 121 MNDKGELYGSEKLTSECIFREQFEENWNTYSSNLYKHGDTGRRYFVALNKDGTPRDGR 180
DB 121 MNDKGELYGSEKLTSECIFREQFEENWNTYSSNLYKHGDTGRRYFVALNKDGTPRDGR 180

QY 181 SKRHQKFTFLPRPDPKVPPELYKDLLMYT 211
DB 181 SKRHQKFTFLPRPDPKVPPELYKDLLVIT 211

RESULT 3
JC7082
fibroblast somatotropin-20 - African clawed frog
N:Alternate names: fibroblast growth factor-20
C:Species: Xenopus laevis (African clawed frog)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: JC7082
R:Koga, C.; Adati, N.; Nakata, K.; Mikoshiba, K.; Furuhashi, Y.; Sato, S.; Tei, H.; Sakak
Biochem. Biophys. Res. Commun. 261, 756-765, 1999
A:Title: Characterization of a novel member of the FGF family, XFGF-20, in Xenopus laevi
A:Reference number: JC7082; MUID:99373151
A:Molecule type: mRNA
A:Accession: JC7082
A:Residues: 1-208 <KOG>
A:Cross-references: DDBJ:AB012615; NID:g5762261; PIDN:BAAG3474.1; PID:g5762262
C:Superfamily: fibroblast growth factor
C:Keywords: differentiation; fibroblast; growth factor; heparin binding

Query Match      80.9%; Score 904.5; DB 2; Length 208;
Best Local Similarity 80.6%; Pred. No. 1.4e-77;
Matches 170; Conservative 19; Mismatches 19; Indels 3; Gaps 2;

QY 1 MAPLAEVGGFLGGLGQVGSFLLPPAGERPPLLGERRSAAERSARGGPGAAQLAHL 60
DB 1 MAPLADVGTFLGGLGQVGSFLLPPAGERPPLLGERRSAP--SDLSHL 57

QY 61 HGLRRRLQYCRGTGFHLQILPDGVSQGTRODHSFLGILEFISVAVGLVSRGVDSGLYL 120
DB 58 QGLRRRLQYCRGTGFHLQILPDGVSQGTRODHSRFGILEFISVAVGLVSRGVDTGLYL 117

QY 121 MNDKGELYGSEKLTSECIFREQFEENWNTYSSNLYKHGDTGRRYFVALNKDGTPRDGR 180
DB 118 MNDKGELYGSEKLTSECIFREQFEENWNTYSSNLYKHGDSRRYFVALNKDGTPRDGT 177

QY 181 SKRHQKFTFLPRPDPKVPPELYKDLLMYT 211
DB 178 AKRHQKFTFLPRPDPKVPPELYKDLGYS 208

RESULT 4
S66486
fibroblast growth factor 9 - mouse
A:Contents: Mus musculus (house mouse)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S66486
R:Seo, M.; Noguichi, K.
FEBS Lett. 370, 231-235, 1995
A:Title: Retinoic acid induces gene expression of fibroblast growth factor-9 during i
A:Reference number: S66486; MUID:95385801
A:Accession: S66486
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-208 <SEO>
A:Cross-references: EMBL:D38258; NID:g1107458; PIDN:BAAG7410.1; PID:g1107459
C:Superfamily: fibroblast growth factor

Query Match      69.3%; Score 774.5; DB 2; Length 208;
Best Local Similarity 70.6%; Pred. No. 2.4e-65;
Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;

QY 1 MAPLAEVGGFLGGLGQVGSFLLPPAGERPPLLGERRSAAERSARG--GPGAAQL 57
DB 1 MAPLGEVGSYFGVQDAV--PFGNVPVLPV--DSPVLLSDHLGQSE--AGGLPRGPAVTDL 54

QY 58 AHLGILRRRLQYCRGTGFHLQILPDGVSQGTRODHSFLGILEFISVAVGLVSRGVDSGL 117
DB 55 DHLKILRRRLQYCRGTGFHLEIFPNGTIQGTRKDHRSRFGILEFISVAVGLVSRGVDSGL 114

QY 118 YLGMNDKGELYGSEKLTSECIFREQFEENWNTYSSNLYKHGDTGRRYFVALNKDGT 177
DB 115 YLGNNEKELYGSEKLTQECVFREQFEENWNTYSSNLYKHVDTRRYVVALNKDGT 174

QY 178 GARSKRHKFTFLPRPDPKVPPELYKDLL 208
DB 175 GTRTKRHQKFTFLPRPDPKVPPELYKDL 205

RESULT 5
A48137
fibroblast growth factor 9 - human
N:Alternate names: glia-activating factor
C:Species: Homo sapiens (man)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: A48137
R:Miyaamoto, M.; Naruo, K.; Seko, C.; Matsumoto, S.; Kondo, T.; Kurokawa, T.
Mol. Cell. Biol. 13, 4251-4259, 1993
A:Title: Molecular cloning of a novel cytokine cDNA encoding the ninth member of the
A:Reference number: A48137; MUID:93309459
A:Accession: A48137
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-208 <MIY>
A:Cross-references: GB:D14838; NID:g391718; PIDN:BAAG3572.1; PID:g391719
A:Experimental source: foreskin
A>Note: sequence extracted from NCBI backbone (NCBIN:134640, NCBIIP:134641)
C:Genetics:
A:Gene: GDB:FGF9
A:Cross-references: GDB:207221; OMIM:600921
A:Map position: 13q11-13q12
C:Superfamily: fibroblast growth factor

Query Match      69.3%; Score 774.5; DB 2; Length 208;
Best Local Similarity 70.6%; Pred. No. 2.4e-65;
Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;

QY 1 MAPLAEVGGFLGGLGQVGSFLLPPAGERPPLLGERRSAAERSARG--GPGAAQL 57
DB 1 MAPLGEVGNVFGVQDAV--PFGNVPVLPV--DSPVLLSDHLGQSE--AGGLPRGPAVTDL 54

QY 58 AHLGILRRRLQYCRGTGFHLQILPDGVSQGTRODHSFLGILEFISVAVGLVSRGVDSGL 117
DB 55 DHLKILRRRLQYCRGTGFHLEIFPNGTIQGTRKDHRSRFGILEFISVAVGLVSRGVDSGL 114

QY 118 YLGMNDKGELYGSEKLTSECIFREQFEENWNTYSSNLYKHGDTGRRYFVALNKDGT 177
DB 115 YLGNNEKELYGSEKLTSECIFREQFEENWNTYSSNLYKHVDTRRYVVALNKDGT 174
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Db	115	YLGMEKEGLVSEKLTQECVFREQEENWYTYSSNLKKYHDIGRRYYVALNKDGTPE	174
QY	178	GASRKRHQKTFTHLPRPVDPERPVELYKOLL	208
Db	175	GPTRKRHQKTFTHLPRPVDPKQVPELYKOLL	205

RESULT 6
JC5941
fibroblast growth factor 16 - human
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C/Accession: JC5941
R: Miyake, A.; Koniishi, M.; Martin, F.H.; Hernday, N.A.; Ozaki, K.; Yanamoto, S.; Mikami, B.; Biochem. Biophys. Res. Commun. 243, 148-152, 1998
A/Title: Structure and expression of a novel member, FGF-16, of the fibroblast growth factor family
A/Reference number: JC5940; MUID:98139883
A/Accession: JC5941
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-207 <MIY>
A/Cross-references: DDBJ:AB000391; NID:G2911169; PTDN:BAA24956.1; PID:g2911170
C/Superfamily: fibroblast growth factor

Query Match	63.4%;	Score 708.5;	DB 2;	Length 207;
Best Local Similarity	63.2%;	Pred. No. 3.8e-59;		
Matches 134;	Conservative	27;	Mismatches 40;	Indels 11; Gaps 4;

Qy	4	LAEVGGFGLGLE---	GLGQOVCSHELLPACERPP	LCGRSAAE--RSARGGPCAQLA	58		
Db	1	MAEVGGVFASLDWD	LHGCFSSSLG---	VPLADSEGF	LCGRSGP--TDFA	54	
Qy	59	HLHGILRRRLQYCR	TGTHLQTLDPG	SVQGTRODHSLEF	LFTISVAVGLVSIRGVDSGLY	118	
Db	55	HLKGILRRRLQYCR	TGTHLEFPNGV	HGTHDHSRFGLEF	ISUAVGLISIRGVDSGLY	114	
Qy	119	LGNNDKGELYSEK	LTSICIFRQF	QFENWNTYSSNIYKHG	DGTRRYEVALNKDGT	PROG	178
Db	115	LCMNERGELYSK	LTRCYRQF	QFENWNTYAS	LYKHSDSRQYVVALNKD	SPREG	174
Qy	179	AKSKRHQFTFL	PRPVDPRV	ELYKDLIMY		210	
Db	175	YTKRHQKFTFL	PRPVDPSK	LSMSRDLFHY		206	

RESULT 7
JC5940
fibroblast growth factor 16 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: JC5940
R:Miyaake, A.; Konishi, M.; Martin, F.H.; Hernday, N.A.; Ozaki, K.; Yamamoto, S.; Mikami,
Biochem. Biophys. Res. Commun. 243, 148-152, 1998
A:Title: Structure and expression of a novel member, FGF-16, of the fibroblast growth factor
A:Reference number: JC5940; MUID:98139883
A:Accession: JC5940
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-207 <MIY>
A:Cross-references: DDBJ:AB002561; NID:G2911149; PIDN:BAA24947.1; PID:G2911150
C:Superfamily: fibroblast growth factor

Query Match 63.1%; Score 705.5; DB 2; Length 207;
Best Local Similarity 62.7%; Pred. No. 7.3e-59;
Matches 133; Conservative 28; Mismatches 40; Indels 11; Gaps 4;

QY	4	LAEVGGFLGG----	LEG LGQOVGSHFLL	PAGERPPLLCERSAAE	RSARGGPGAQILA	58
			:	:	:	
Db	1	MAEVGGFASLWD	LQGFSSJG----	VELADSGFLNERLQ	LEGKLQKRGSP--	TDFA 54
			:	:	:	
QY	59	HLHGILRRQLYCR	TGTHQLQPLDQGS	QQTGRQDHSFLGFL	ETISVAVGLVIRG	WDSGLY 118
			:	:	:	
Db	55	HLKGLIRRRQLYCR	TGTHFLFFNGTVH	GRPHDSRFGLEFI	LSVAVGLVIRG	WDSGLY 114
			:	:	:	

Qy	119	LGMDKGE	LGSGE	SKL	ISEC	IFRQ	PEN	WNT	YSS	NIY	XHG	D	TGR	YF	VAL	KNK	D	T	PDG	178				
Db	115	LGMMERGE	LGSKL	L	REC	VF	REQ	FEN	WNT	Y	TAS	T	Y	KL	S	ERQ	Y	Y	VAL	KNK	D	SPRG	174	
Qy	179	ARSKRHQ	K	TF	LP	VP	D	PE	K	VP	EL	X	K	L	L	M	Y							210
Db	175	YRTKRH	Q	K	H	Q	K	T	F	LP	VP	D	S	K	L	S	M	S	R	D	L	F	R	206

RESULT 8
I50588
fibroblast growth factor 3 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 17-Mar-2000
C:Accession: I50588
R:Mahmood, R.; Klefer, P.; Guthrie, S.; Dickson, C.; Mason, I.
Development 121, 1399-1410, 1995
A:Title: Multiple roles for FGF-3 during cranial neural development in the chicken.
A:Reference number: I50588; MUID:95309122
A:Accession: I50588
A:Status: preliminary; translated from GB/EMBL/DDBT
A:Molecule type: mRNA
A:Residues: 1-220 <NAH>
A:Cross-references: EMBL:Z47555; NID:g623215; PIDN:CAA87635.1; PID:g623216
C:Superfamily: fibroblast growth factor

Query Match 30.6%; Score 342.5; DB 2; Length 220;
Best Local Similarity 41.6%; Pred. No. 1e-24;
Matches 77; Conservative 29; Mismatches 56; Indels 23; Gaps 4;

[illegible]

```

RESULT 9
S68144
fibroblast growth factor 5 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S68144
R:Hattori, Y.; Yamasaki, M.; Itoh, N.
Biochim. Biophys. Acta 1306, 31-33, 1996
A:Title: The rat FGF-5 mRNA variant generated by alternative splicing encoded
A:Reference number: S68144; MUID:96201703
A:Accession: S68144
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-266 <HAT>
A:Cross-references: EMBL:D64085; NID:g992952; PIDN:RAA10966.1; PID:g992953
C:Superfamily: fibroblast growth factor

```

Query Match	29.0%;	Score 324.5;	DB 2;	Length 266;
Best Local Similarity	39.8%;	Pred. No. 6.6e-23;		
Matches	86;	Conservative	24;	Mismatches 69;
			Indels	37;
			Gaps	9;

Qy 23 SHFTLL--PPAGER-----PP-----LLGER-----RSAAESARGGPGAAQLA 58
||:|:||: || || || ||:| ||:|

D6 12 SHLLLSAPAOGEKRLTPEGOPAPRPNPGDSSGRGRSATFASSSASSPPVAASPGSGSG 71
||:|:||: || || || ||:| ||:|

N:Alternate names: transforming protein int-2
C:Species: homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Sep-1999
C:Accession: S04742
R:Brookes, S.; Smith, R.; Casey, G.; Dixon, M.; Peters, G.
Oncogene 4, 429-436, 1989
A:Title: Sequence organization of the human int-2 gene and its expression in teratocarcinoma
A:Reference number: S04742; MUID:89239468
A:Accession: S04742
A:Molecule type: DNA
A:Residues: 1-239 <BROS>
A:Cross-references: EMBL:X14445; NID:g33937; PIDN:CAA32615.1; PID:g312409
C:Genetics:
A:Gene: GDB:FGF3; INT2
A:Cross-references: GDB:120103; OMIM:164950
A:Map position: 11q13.3-11q13.3
A:Introns: 74/1; 108/3
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-239/Product: transforming protein (int-2) #status predicted <MAT>

Query Match 28.5%; Score 319; DB 1; Length 239;
Best Local Similarity 41.1%; Pred. No. 1.9e-22;
Matches 78; Conservative 29; Mismatches 61; Indels 22; Gaps 6;

QY 28 PAGERPPPLIGERRSAERSARGGGAQAHLHGLRRRLRYCFTGPHLQILPDGSGVQG 87
Db 17 PAAGPGARL---RRDA-----GGRGGV-YEHLGGAPRRKLYCATYHQLHPSGRVNG 66

QY 88 TRQDHLGFLGIFISVAVGLVIRGVDSGLYGMNDKGLYSEKLTSECFRQFEENW 147
Db 67 S-LENSAYSILEITAVEGIVAIRGLFSGRVLANMKRGLYASAECEFEVERIHELG 125

QY 148 YNTYSSNIY-----KHGDTGRRYFVALNKDGTDPDGAARKHQKFTHFLPRVDP 197
Db 126 YNTYASRLYTVSSTPGARRQPSAERLWYVSVNGKRRPGRGFKTRTQKSLFLPRVLD- 184

QY 198 ERVPELYKDL 207
Db 185 HRDHENVRQL 194

RESULT 14
TVMST2
A:Title: transforming protein (int-2) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 18-Jun-1999
C:Accession: A23930; S08157
R:Moore, R.; Casey, G.; Brookes, S.; Dixon, M.; Peters, G.; Dixon, C.
EMBO J. 5, 919-924, 1986
A:Title: Sequence, topography and protein coding potential of mouse int-2: a putative on-
cogene
A:Reference number: A23930; MUID:86247582
A:Accession: A23930
A:Molecule type: DNA; mRNA
A:Residues: 1-245 <MOO>
A:Cross-references: GB:X00848; GB:X26284; GB:X68450; NID:g52716; PIDN:CAA68767.1; PID:g5
R:Acland, P.; Dixon, M.; Peters, G.; Dixon, C.
Nature 343, 662-665, 1990
A:Title: Subcellular fate of the Int-2 oncoprotein is determined by choice of initiation
A:Reference number: S08157; MUID:90158795
A:Accession: S08157
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 'HSRAGLARGVLPAPRLRETRACAAAAGGRDAGM', 3-17 <ACL>
C:Genetics:
A:Gene: int-2
A:Map position: 7
A:Introns: 74/1; 108/3
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor; transforming protein

Query Match 28.4%; Score 317; DB 1; Length 245;

Best Local Similarity 43.0%; Pred. No. 3e-22;
Matches 68; Conservative 28; Mismatches 50; Indels 12; Gaps 3;

QY 46 RSARGPGAAQLAHLHGLRRRLRYCFTGPHLQILPDGSGVOGTRODHSLEIFTSVAV 105
Db 26 RRDAGRGGV-YEHLGGAPRRKLYCATYHQLHPSGRVNGS-LENSAYSILEITAVEV 83

QY 106 GLVSRGVDSGLYGMNDKGLYSEKLTSECFRQFEENWYNTYSSNIYKHGDTG--- 162
Db 84 GVVAIKGLFSGRVLANMKRGLYASDHNAECEFVERIHELGYNTYASRLYRTGSSGPGA 143

QY 163 -----RRYFVALNKDGTDPDGAARKHQKFTHFLPR 193
Db 144 QRQGAQRPWYVSVNGKRRPGRGFKTRTQKSLFLPR 181

RESULT 15
JC4627
A:Title: fibroblast growth factor 3 - zebra fish
C:Species: Brachydanio rerio (zebra fish)
C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 16-Jul-1999
C:Accession: JC4627
R:Kiefer, P.; Straehle, U.; Dickson, C.
Gene 168, 211-215, 1996
A:Title: The zebrafish Fgf-3 gene: cDNA sequence, transcript structure and genomic or-
ganization
A:Reference number: JC4627; MUID:96194899
A:Accession: JC4627
A:Molecule type: mRNA
A:Residues: 1-256 <KIE>
A:Cross-references: EMBL:Z48714; NID:g971333; PIDN:CAA88596.1; PID:g971334
A:Experimental source: embryo
A:Note: The authors translated the codon TGG for residue 178 as His
C:Comment: This factor belongs to the fibroblast growth factor family which have the
protein is a cell signalling molecule and plays the roles during the early stages of de-
velopment
A:Gene: Fgf-3
A:Introns: 93/2; 127/3
C:Superfamily: fibroblast growth factor
C:Keywords: embryo; fibroblast; growth factor

Query Match 27.5%; Score 307; DB 2; Length 256;
Best Local Similarity 37.0%; Pred. No. 2.8e-21;
Matches 70; Conservative 33; Mismatches 66; Indels 20; Gaps 3;

QY 34 PPLLGERSAERSARGGGAQAHLHGLRRRLRYCFTGPHLQILPDGSGVOGTRODHS 93
Db 32 PCARGQACDPQRORDAGRGGV-YEHLGGAPRRKLYCATYHQLHPSGRVNGSLENN 90

QY 94 LFGILEFTSVAVGLVIRGVDSGLYGMNDKGLYSEKLTSECFRQFEENWYNTYSS 153
Db 91 PLSILEITAVDGVVAIKGLFSGRVLANMKRGLYASDHNAECEFVERIHELGYNTYAS 150

QY 154 NIY-----KHGDTGRRYFVALNKDGTDPDGAARKHQKFTHFLPRV-- 195
Db 151 RHHTATQPPPTGGSGIGGSKRRASSKRWVSVNGKRRPGRGFKTRTQKSLFLPRVLN 210

QY 196 -DPERVPEL 203
Db 211 KOHEMVRKL 219

Search completed: October 21, 2002, 16:15:34
Job time : 22 secs


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QY 61 HGILRRRLCYRTGFHLQILPDGSGVOGTRODHSFLGILEFTISVAVGLVSTIRGVDSGLYL 120
Db 61 HGILRRRLCYRTGFHLQILPDGSGVOGTRODHSFLGILEFTISVAVGLVSTIRGVDSGLYL 120
QY 121 MNDKGLYGSSEKLTSECFRQFEENWNTYSSNIYKHGDTGRYFVALNKDCTPRDGR 180
Db 121 MNDKGLYGSSEKLTSECFRQFEENWNTYSSNIYKHGDTGRYFVALNKDCTPRDGR 180
QY 181 SKRHOKFTFLPRVPDPRVPELYKDLMLYT 211
Db 181 SKRHOKFTFLPRVPDPRVPELYKDLMLYT 211

RESULT 2
FGF9_HUMAN
ID FGF9_HUMAN STANDARD; PRT; 208 AA.
AC P31371;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glia-activating factor precursor (GAF) (Fibroblast growth factor-9)
DE (FGF-9) (HBGF-9).
OS FGF9.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Foreskin;
RX MEDLINE=93309459; PubMed=8321227;
RA Miyamoto M., Naruo K.-I., Seko C., Matsumoto S., Kondo T.,
RA Kurokawa T.;
RT "Molecular cloning of a novel cytokine cDNA encoding the ninth member
RT of the fibroblast growth factor family, which has a unique secretion
RT property.";
RL Mol. Cell. Biol. 13:4251-4259(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Blakey S.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 4-26 AND 34-54.
RC TISSUE=Glia; tumor;
RX MEDLINE=9315105; PubMed=8428960;
RA Naruo K.-I., Seko C., Kuroshima K.-I., Matsutani E., Sasada R.,
RA Kondo T., Kurokawa T.;
RT "Novel secretory heparin-binding factors from human glioma cells
RT (glia-activating factors) involved in glial cell growth.
RT Purification and biological properties.";
RL J. Biol. Chem. 268:2857-2864(1993).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.60 ANGSTROMS).
RX MEDLINE=21127675; PubMed=11223514;
RA Hecht H.J., Adar R., Hofmann B., Bogin O., Welch H., Yayon A.;
RT "Structure of fibroblast growth factor 9 shows a symmetric dimer with
RT unique receptor- and heparin-binding interfaces.";
RL Acta Crystallogr. D 57:378-384(2001).
CC -1- FUNCTION: MAY HAVE A ROLE IN GLIAL CELL GROWTH AND DIFFERENTIATION
CC DURING DEVELOPMENT, GLIOSIS DURING REPAIR AND REGENERATION OF
CC BRAIN TISSUE AFTER DAMAGE, DIFFERENTIATION AND SURVIVAL OF
CC NEURONAL CELLS, AND GROWTH STIMULATION OF GLIAL TUMORS.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: GLIAL CELLS.
CC -1- PTM: THREE MOLECULAR SPECIES WERE FOUND (30 KDA, 29 KDA AND 25
CC KDA), CLEAVED AT LEU-4, VAL-13 AND SER-34 RESPECTIVELY. THE
CC SMALLER ONES MIGHT BE PRODUCTS OF PROTEOLYTIC DIGESTION.
CC FURTHERMORE, THERE MAY BE A FUNCTIONAL SIGNAL SEQUENCE IN THE 30
CC KDA SPECIES WHICH IS UNCLEAVABLE IN THE SECRETION STEP.
CC -1- PTM: N-GLYCOSYLATED.
CC -1- DISEASE: THE CONTINUOUS OVEREXPRESSION OF GAFS MAY LEAD TO

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CC MALIGANT CELL GROWTH CAUSED BY AN AUTOCRINE LOOP.
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC -1- DATABASE: NAME-R&D Systems' cytokine source book: FGF9;
CC WWW="http://www.rndsystems.com/asp/q_sitebuilder.asp?bodyId=199".
CC -----
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CC -----
CC EMBL; D14838; BAA03572.1; -
CC EMBL; AL139378; CAC17692.1; -
CC PIR; A48137; A48137.
CC PDB; 1G82; 07-MAR-01.
CC MIN; 600921; -
CC InterPro; IPR002209; HBGF_FGF.
CC InterPro; IPR002348; IL1_HBGF.
CC Pfam; PF00167; FGF_1.
CC PRINTS; PR00262; IL1HBGF.
CC PRODOM; PD000831; HBGF_FGF; 1.
CC SMART; SM00442; FGF; 1.
CC PROSITE; PS00247; HBGF_FGF; 1.
CC Growth factor; Differentiation; Mitogen; Heparin-binding;
KW Glycoprotein; 3D-structure.
FT PROPEP 1 3 GLIA-ACTIVATING FACTOR.
FT CHAIN 4 208
FT CARBOHYD 79 79 N-LINKED (GLCNAC. .).
FT CONFLICT 24 26 VLP -> SLL (IN REF. 2).
FT CONFLICT 34 34 S -> A (IN REF. 2).
SQ SEQUENCE 208 AA; 23440 MW; F32A0E7106EF59C9 CRC64;

Query Match 69.3%; Score 774.5; DB 1; Length 208;
Best Local Similarity 70.6%; Pred. No. 1.9e-65;
Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;

QY 1 MAPLAEVGGFLGLEGQQVGSFHLPPAGERPPLIGERRSAAERSARG--GPGAAQL 57
Db 1 MAPLCEVGNVFCQDAV--PFGNVPVLPV--DSPVLLSDHLGQSE--AGGLPRGPAVTDL 54
QY 58 AHLHGILRRRLCYRTGFHLQILPDGSGVOGTRODHSFLGILEFTISVAVGLVSTIRGVDSGL 117
Db 55 DHLKGILRRRLCYRTGFHLGILEFTISVAVGLVSTIRGVDSGL 114
QY 118 YLGMNDKGLYGSSEKLTSECFRQFEENWNTYSSNIYKHGDTGRYFVALNKDCTPRD 177
Db 115 YLGMNEKGLYGSSEKLTQECVFRQFEENWNTYSSNIYKHVDTRRYVVALNKDGTRE 174
QY 178 GARSKRHOKFTFLPRVPDPRVPELYKDLL 208
Db 175 GTRTKRHOKFTFLPRVPDPRVPELYKDLL 205

RESULT 3
FGF9_MOUSE
ID FGF9_MOUSE STANDARD; PRT; 208 AA.
AC P54130;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glia-activating factor precursor (GAF) (Fibroblast growth factor-9)
DE (FGF-9) (HBGF-9).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB;
RX MEDLINE=961139512; PubMed=8576175;

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RA Santos-Ocampo S., Colvin J.S., Chelliah A.T., Ornitz D.M.:
RT "Expression and biological activity of mouse fibroblast growth
RT factor-9".
RN J. Biol. Chem. 271:1726-1731(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95385801; PubMed=7656983;
RA Seo M., Noguichi K.;
RT "Retinoic acid induces gene expression of fibroblast growth factor-9
RT during induction of neuronal differentiation of mouse embryonal
RT carcinoma F19 cells".
RL FEBS Lett. 370:231-235(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96192599; PubMed=8619928;
RA Hecht D., Zimmerman N., Bedford M., Avivi A., Yayon A.;
RT "Identification of fibroblast growth factor 9 (FGF9) as a high
RT affinity, heparin dependent ligand for FGF receptors 3 and 2 but not
RT for FGF receptors 1 and 4".
RL Growth factors 12:223-233(1995).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SVJ;
RA Colvin J.S., Feldman B., Nadeau J.H., Goldfarb M., Ornitz D.M.;
RT "Genomic organization and embryonic expression of the mouse fibroblast
RT growth factor 9 gene".
RN Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY HAVE A ROLE IN GLIAL CELL GROWTH AND DIFFERENTIATION
CC DURING DEVELOPMENT, GLOSTIS DURING REPAIR AND REGENERATION OF
CC BRAIN TISSUE AFTER DAMAGE, DIFFERENTIATION AND SURVIVAL OF
CC NEURONAL CELLS, AND GROWTH STIMULATION OF GLIAL TUMORS.
CC -!- SUBCELLULAR LOCATION: Secreted
CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC
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CC
CC EMBL; U33535; AAC52529.1; -.
CC DR EMBL; D38258; BAA07410.1; -.
CC DR EMBL; S82023; AAB36429.1; -.
CC DR EMBL; AF144626; AAD49222.1; -.
CC DR EMBL; AF144624; AAD49222.1; JOINED.
CC DR EMBL; AF144625; AAD49222.1; JOINED.
CC DR HSSP; P05230; 2ARF.
CC DR MGD; MGI:104723; Fgf9.
CC DR InterPro; IPR002209; HBGF_FGF.
CC DR InterPro; IPR002348; IL1_HBGF.
CC DR Pfam; PF00167; FGF; 1.
CC DR PRINTS; PR00262; ILIHBGF.
CC DR ProDom; PD000831; HBGF_FGF; 1.
CC DR SMART; SM00442; FGF; 1.
CC DR PROSITE; PS00247; HBGF_FGF; 1.
KW Growth factor; Differentiation; Mitogen; Heparin-binding;
FT Glycoprotein.
FT PROPEP 1 3 BY SIMILARITY.
FT CHAIN 4 208 GLIA-ACTIVATING FACTOR.
FT CARBOHYD 79 79 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 208 AA; 23440 MW; E8DE1EEFB70979E CRC64;

Query Match 69.3%; Score 774.5; DB 1; Length 208;
Best Local Similarity 70.6%; Pred. No. 1.9e-65;
Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;

QY 1 MAPLAEVGGFLGSLGQGVCSHPLLPACGERPPLICERSAERSARG---CPGAQL 57
Db 1 MAPLAEVGSYFGVQDAV--PFGNVPFLPV--DSPVLLMDHLGQSE--AGGLPRGPATDDL 54
QY 58 AHLHGILRRQLYCRGTGFHLQILPDGVSQGTQRQDSLFGILEFTSVAVGLSVIRGVDSSL 117

Db 55 DHLKGLRRQLYCRGTGFHLQILPDGVSQGTQRQDSLFGILEFTSVAVGLSVIRGVDSSL 114
QY 118 YLGMDKGLYSEKLTSECTFROFENWYNTSSNYKHGDTGRFYFVALNKDGTGPRD 177
Db 115 YLGMDKGLYSEKLTSECTFROFENWYNTSSNYKHGDTGRFYFVALNKDGTGPRD 174
QY 178 GARSRRHKQFTHLPVPDPVDPVPELYKDLL 208
Db 175 GTRTRHKQFTHLPVPDPVDPVPELYKDLL 205

RESULT 4
FGF9_RAT
ID FGF9_RAT STANDARD; PRT; 208 AA.
AC P36364;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Glia-activating factor precursor (GAF) (Fibroblast growth factor-9)
DE (FGF-9) (HBGF-9).
GN FGF9 OR FGF-9.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93309459; PubMed=8321227;
RA Miyamoto M., Naruo K.-I., Seko C., Matsumoto S., Kondo T.,
RA Kurokawa T.;
RT "Molecular cloning of a novel cytokine cDNA encoding the ninth member
RT of the fibroblast growth factor family, which has a unique secretion
RT property".
RL Mol. Cell. Biol. 13:4251-4259(1993).
CC -!- FUNCTION: MAY HAVE A ROLE IN GLIAL CELL GROWTH AND DIFFERENTIATION
CC DURING DEVELOPMENT, GLOSTIS DURING REPAIR AND REGENERATION OF
CC BRAIN TISSUE AFTER DAMAGE, DIFFERENTIATION AND SURVIVAL OF
CC NEURONAL CELLS, AND GROWTH STIMULATION OF GLIAL TUMORS.
CC -!- SUBCELLULAR LOCATION: Secreted
CC -!- TISSUE SPECIFICITY: BRAIN AND KIDNEY.
CC -!- PTM: N-GLYCOSYLATED.
CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC
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CC
CC EMBL; D14839; BAA03573.1; -.
CC DR HSSP; P05230; 2ARF.
CC DR InterPro; IPR002209; HBGF_FGF.
CC DR InterPro; IPR002348; IL1_HBGF.
CC DR Pfam; PF00167; FGF; 1.
CC DR PRINTS; PR00262; ILIHBGF.
CC DR ProDom; PD000831; HBGF_FGF; 1.
CC DR SMART; SM00442; FGF; 1.
CC DR PROSITE; PS00247; HBGF_FGF; 1.
KW Growth factor; Differentiation; Mitogen; Heparin-binding;
FT Glycoprotein.
FT PROPEP 1 3 BY SIMILARITY.
FT CHAIN 4 208 GLIA-ACTIVATING FACTOR.
FT CARBOHYD 79 79 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 208 AA; 23413 MW; 4A3CB894DF643EB CRC64;

Query Match 69.3%; Score 774.5; DB 1; Length 208;
Best Local Similarity 70.6%; Pred. No. 1.9e-65;
Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;

```
OY 1 MAPLAEVGGFLGGLGQQVSGSHFLPPACGERPILLGERSAARSARG---GPGAAQL 57
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 MAPLGEVSGYFGVQDAV--PFGNVPLV--DSPVLLSDHLGQSE--AGGLPRGPATVDL 54
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 58 AHLHGILRRRLQYCRGTGFLHQLTLDGSGVQGTRODHSILFGLFISVAVGLVSRGVDSGL 117
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 55 DHLKGILRRRLQYCRGTGFLHQLTLDGSGVQGTRODHSILFGLFISVAVGLVSRGVDSGL 114
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 118 YLGMNDKGLYGSEKLTSECIFREQFEENWYNTSSNIYKHGDTGRRYFVALNKDGTPRD 177
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 115 YLGMNEKGLYGSEKLTCECVFREQFEENWYNTSSNLYKHVDTGRRYFVALNKDGTPRE 174
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 178 GARSKRHKQKFTFLPRPDPVDPVPELYKOLL 208
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 175 GTRTKRHKQKFTFLPRPDPVDPVPELYKOLL 205
| : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
FGF9_XENLA
ID FGF9_XENLA STANDARD; PRT; 209 AA.
AC Q91875;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Glia-activating factor precursor (GAF) (Fibroblast growth factor-9)
DE (FGF-9) (HBGF-9) (XFGF-9).
GN FGF9.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97006698; PubMed=8853991;
RA Song J., Slack J.M.W.;
RT "XFGF-9; a new fibroblast growth factor from Xenopus embryos.";
RL Dev. Dyn. 206:427-436(1996).
CC -!- FUNCTION: MAY HAVE A ROLE IN MUSCLE DEVELOPMENT AND NEURAL
CC DIFFERENTIATION, HAS NO SPECIFIC ROLE IN ANTEROPOSTERIOR
CC PATTERNING.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: MATERNAL TRANSCRIPT IS FOUND MAINLY IN THE
CC ANIMAL HEMISPHERE. ZYGOTIC TRANSCRIPT IS FOUND AROUND THE
CC BLASTOPORE AND IN THE LATE GASTRULA STAGE, IN THE DORSAL PART. IN
CC LATER STAGES IT IS FOUND ALONG THE DORSAL PART AND HEAD REGION.
CC -!- DEVELOPMENTAL STAGE: THE MATERNAL PROTEIN IS DETECTED UP TO THE
CC BLASTULA STAGE BUT DECLINES BY THE EARLY GLASTRULA. ZYGOTIC
CC EXPRESSION STARTS AT AROUND EARLY GASTRULA; THE LEVEL OF
CC EXPRESSION REACHED AT STAGE 15 PERSISTS DURING NEURULA AND TAILBUD
CC STAGES, AND IS FURTHER INCREASED DURING THE TADPOLE STAGES.
CC -!- PTM: KNOWN TO BE GLYCOSYLATED.
CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC
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FT PROPP 1 3 BY SIMILARITY.
FT CHAIN 4 209 GLIA-ACTIVATING FACTOR.
FT CARBOHYD 80 80 N-LINKED (GLCNAC...) (PROBABLE).
FT SEQUENCE 209 AA; 23662 MW; 26CBB229797FCBF CRC64;

Query Match 68.4%; Score 765; DB 1; Length 209;
Best Local Similarity 70.1%; Pred. No. 1.5e-64;
Matches 148; Conservative 16; Mismatches 39; Indels 8; Gaps 2;

OY 1 MAPLAEVGGFLGGLGQQVSGSHFLPPACGERPILLGERSAARSARG---GPGAAQL 57
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 MAPLGEVGNVFG-----VQDAVSGNVPLVQDTPVLLSDHMSHSEAGLPRGSATVDL 55
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 58 AHLHGILRRRLQYCRGTGFLHQLTLDGSGVQGTRODHSILFGLFISVAVGLVSRGVDSGL 117
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 56 EHLKGILRRRLQYCRGTGFLHQLTLDGSGVQGTRODHSILFGLFISVAVGLVSRGVDSGL 115
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 118 YLGMNDKGLYGSEKLTSECIFREQFEENWYNTSSNIYKHGDTGRRYFVALNKDGTPRD 177
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 116 YLGMNEKGLYGSEKLTCECVFREQFEENWYNTSSNLYKHADTGRRYFVALNKDGTSRD 175
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 178 GARSKRHKQKFTFLPRPDPVDPVPELYKOLL 208
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 176 GTRTKRHKQKFTFLPRPDPVDPVPELYKOLL 206
| : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
FGF9_HUMAN
ID FGF9_HUMAN STANDARD; PRT; 207 AA.
AC Q43320;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fibroblast growth factor-16 (FGF-16).
GN FGF16.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Heart;
RX MEDLINE=98139883; PubMed=9473496;
RA Miyake A., Konishi M., Martin F.H., Hernday N.A., Ozaki K.,
RA Yamamoto S., Mikami T., Arakawa T., Itoh N.;
RT "Structure and expression of a novel member, FGF-16, on the fibroblast
RT growth factor family.";
RL Biochem. Biophys. Res. Commun. 243:148-152(1998).
CC -!- FUNCTION: INDUCES HEPATOCELLULAR PROLIFERATION. HAS NO BIOLOGICAL
CC -!- EFFECT ON THE HEART (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted (by similarity).
CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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KW Growth factor; Mitogen; Signal; Glycoprotein.
FT SIGNAL 1 21
FT CHAIN 22 237 FIBROBLAST GROWTH FACTOR-3.
FT CARBOHYD 83 83 N-LINKED (GLCNAC...).
SQ SEQUENCE 237 AA; 26984 MW; EDD31B0893567A2D CRC64;

Query Match 29.0%; Score 324; DB 1; Length 237;
Best Local Similarity 40.6%; Pred. No. 3.3e-23;
Matches 73; Conservative 29; Mismatches 62; Indels 16; Gaps 3;

QY 32 ERPPLL-----GERRSAERSARGPGAAQLAHLHILRRRLQYKRTGFHLQILPDGVSQ 86
DB 25 EREPKYPCSRGKLCDFQRDRAGRGV-YEHLGAPNRKLYCATYHQLIHLNGKIN 83
QY 87 GTRQDHSFLGILFISVAVGLVIRGVDGLYGMNDKGLYSGSKLTSETCFRQPPEN 146
DB 84 GTLEKNSVFSLEITAVDVGIVAIGLFGSLYGLAMNQRGLYASETYNPECFEVEIRHEL 143
QY 147 WNTYSSNIYKHGDTG-----RRYFVALNKDGTTPRDGARGKRHKQKTHFLPRVD 196
DB 144 GYNTYASLEYTPVSGAGTKRKASAEALWYVSYNGKRRPRGFKYRRYQKSLFLPRVLD 203

RESULT 11
FGF5_HUMAN
ID FGF5_HUMAN STANDARD; PRT; 268 AA.
AC P12034; 075846;
DT 01-OCT-1989 (Rel. 12, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Fibroblast growth factor-5 precursor (FGF-5) (HBGF-5) (Smag-82).
GN FGF5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Brain stem;
RC MEDLINE=91045929; PubMed=1700424;
RA Haub O., Drucker B., Goldfarb M.;
RT "Expression of the murine fibroblast growth factor 5 gene in the
RT adult central nervous system."
RL Proc. Natl. Acad. Sci. U.S.A. 87:8022-8026(1990).
RN [2]
RP SEQUENCE FROM N.A. (LONG ISOFORM).
RX MEDLINE=8906942; PubMed=3211147;
RA Zhan X., Bates B., Hu X., Goldfarb M.;
RT "The human FGF-5 oncogene encodes a novel protein related to
RT fibroblast growth factors."
RL Mol. Cell. Biol. 8:3487-3495(1988).
RN [3]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RA Ozawa K., Suzuki S., Asada M., Tomooka Y., Li A., Yoneda A., Komi A.,
RA Imanura T.;
RT "An alternatively-spliced FGF-5 mRNA is abundant in brain and
RT translates into a partial agonist/antagonist for FGF-5 neurotrophic
RT activity."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RC TISSUE=Umbilical artery;
RX MEDLINE=20379035; PubMed=10823842;
RA de Vries C.J.M., van Achterberg T.A.E., Horrevorts A.J.G.,
RA ten Cate J.W., Pannekoek H.;
RT "Differential display identification of 40 genes with altered
RT expression in activated human smooth muscle cells. Local expression
RT in atherosclerotic lesions of smags, smooth muscle
RT activation-specific genes."
RL J. Biol. Chem. 275:23939-23947(2000).
CC -!- FUNCTION: THIS ONCOGENE IS EXPRESSED IN NEONATAL BRAIN. FGF-5 CAN
CC TRANSFORM NIH 3T3 CELLS.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
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FGF3_HUMAN
ID FGF3_HUMAN STANDARD; PRT: 239 AA.
AC P11487;
DT 01-OCT-1989 (Rel. 12, Created)
DE 01-OCT-1989 (Rel. 12, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE INT-2 proto-oncogene protein precursor (Fibroblast growth factor-3)
DE (FGF-3) (HBGF-3).
GN FGF3 OR FGF-3 OR INT-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RX MEDLINE=86247582; PubMed=3013624;
RP SEQUENCE FROM N.A.
RA Moore R., Casey G., Brookes S., Dixon M., Peters G., Dickson C.;
RT "Sequence, topology and protein coding potential of mouse int-2: a
RT putative oncogene activated by mouse mammary tumour virus.";
RL EMBO J. 5:919-924(1986).
RN [2]
CC SEQUENCE OF 1-73 FROM N.A.
CC MEDLINE=88296404; PubMed=2841106;
CC Smith R., Peters G., Dickson C.;
CC "Multiple RNAs expressed from the int-2 gene in mouse embryonal
CC carcinoma cell lines encode a protein with homology to fibroblast
CC growth factors."
CC EMBO J. 7:1013-1022(1988).
RN [3]
CC CHARACTERIZATION.
CC MEDLINE=91193291; PubMed=1964688;
CC Dickson C., Acland P., Smith R., Dixon M., Deed R., McAllan D.,
CC Walther W., Fuller-Pace F., Kiefer P., Peters G.;
CC "Characterization of int-2: a member of the fibroblast growth factor
CC family.";
CC J. Cell Sci. Suppl. 13:87-96(1990).
CC -1- FUNCTION: COULD BE INVOLVED IN EAR DEVELOPMENT.
CC -1- INDUCTION: BY INTEGRATION OF MOUSE MAMMARY TUMOR VIRUS.
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: Y00848; CAA68767.1;
CC PIR: A23930; TVMST2.
CC HSP: P09038; IBFG.
CC MIM: 164950;
CC InterPro: IPR002209; HBGF_FGF.
CC InterPro: IPR002348; IL1_HBGF.
CC Pfam: PF00167; FGF_1.
CC PRINTS: PR00262; IL1HBGF.
CC ProDom: PD000831; HBGF_FGF; 1.
CC SMART: SM00442; FGF_1.
CC PROSITE: PS00247; HBGF_FGF; 1.
CC Proto-oncogene; Growth factor; Mitogen; Signal; Glycoprotein.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 239 INT-2 PROTO-ONCOGENE PROTEIN.
FT CARBOHYD 65 65 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 239 AA; 26886 MW; 8DBEF17D2B2E3C63 CRC64;
Query Match 28.5%; Score 319; DB 1; Length 239;
Best Local Similarity 41.1%; Pred. No. 9.8e-23;
Matches 78; Conservative 29; Mismatches 61; Indels 22; Gaps 6;
QY 28 PPAGERPPLGERRSAAERSARGPGAAQLAHLGILRRRLQYCRGTGHLQILPDGSGVQ 87
DQ 17 PAAGPGCARL---RRDA-----GGRGVV-YEHLGGAPRRRKLYCATKYHLQHPGSRVNG 66
QY 88 TRQDHSILGILFISVANGLYSIRVDSGLYLGNNDKGLYSGEKLTSCEIFREQEENW 147
DQ 67 S-LENSAYSILEITAVEGVIAIRGLFSGRYLAANKRGRLYASEHYSACEFVERIHEL 125
QY 148 YNTYSSNIY-----KHGDTGRRYFVALNKDGPVPGARSKRQKFTPLPRPVP 197
DQ 126 YNTYASRLYRTVSTPGARRQPSAERLWVSVNGKPRRGRFTRRTQKSSLELPRLVD- 184
QY 198 ERVPELYKDL 207
DQ 185 HRDHVMYRQL 194
RESULT 15
FGF3_MOUSE
ID FGF3_MOUSE STANDARD; PRT: 245 AA.
AC P05524;
DT 01-NOV-1988 (Rel. 09, Created)
DE 01-NOV-1988 (Rel. 09, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE INT-2 proto-oncogene protein precursor (Fibroblast growth factor-3)
DE (FGF-3) (HBGF-3).
GN FGF3 OR FGF-3 OR INT-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RX MEDLINE=86247582; PubMed=3013624;
RP SEQUENCE FROM N.A.
RA Moore R., Casey G., Brookes S., Dixon M., Peters G., Dickson C.;
RT "Sequence, topology and protein coding potential of mouse int-2: a
RT putative oncogene activated by mouse mammary tumour virus.";
RL EMBO J. 5:919-924(1986).
RN [2]
CC SEQUENCE OF 1-73 FROM N.A.
CC MEDLINE=88296404; PubMed=2841106;
CC Smith R., Peters G., Dickson C.;
CC "Multiple RNAs expressed from the int-2 gene in mouse embryonal
CC carcinoma cell lines encode a protein with homology to fibroblast
CC growth factors."
CC EMBO J. 7:1013-1022(1988).
RN [3]
CC CHARACTERIZATION.
CC MEDLINE=91193291; PubMed=1964688;
CC Dickson C., Acland P., Smith R., Dixon M., Deed R., McAllan D.,
CC Walther W., Fuller-Pace F., Kiefer P., Peters G.;
CC "Characterization of int-2: a member of the fibroblast growth factor
CC family.";
CC J. Cell Sci. Suppl. 13:87-96(1990).
CC -1- FUNCTION: COULD BE INVOLVED IN EAR DEVELOPMENT.
CC -1- INDUCTION: BY INTEGRATION OF MOUSE MAMMARY TUMOR VIRUS.
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: Y00848; CAA68767.1;
CC PIR: A23930; TVMST2.
CC HSP: P09038; IBFG.
CC MIM: 164950;
CC InterPro: IPR002209; HBGF_FGF.
CC InterPro: IPR002348; IL1_HBGF.
CC Pfam: PF00167; FGF_1.
CC PRINTS: PR00262; IL1HBGF.
CC ProDom: PD000831; HBGF_FGF; 1.
CC SMART: SM00442; FGF_1.
CC PROSITE: PS00247; HBGF_FGF; 1.
CC Proto-oncogene; Growth factor; Mitogen; Signal; Glycoprotein.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 245 INT-2 PROTO-ONCOGENE PROTEIN.
FT CARBOHYD 65 65 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 245 AA; 27214 MW; 70D94FD6A7837C79 CRC64;
Query Match 28.4%; Score 317; DB 1; Length 245;
Best Local Similarity 43.0%; Pred. No. 1.6e-22;
Matches 68; Conservative 28; Mismatches 50; Indels 12; Gaps 3;
QY 46 RSARGGPGAAQLAHLGILRRRLQYCRGTGHLQILPDGSGVQTRQDHSILGILFISVAV 105
DQ 26 RRDAGGRGVV-YEHLGGAPRRRKLYCATKYHLQHPGSRVNGS-LENSAYSILEITAVEV 83
QY 106 GLYSIRGVDSGLYLGNNDKGLYSGEKLTSCEIFREQEENWYNTYSSNIYKHGDTG--- 162

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Db 84 GVAIKGLESGRYLAMNKRGLYASDHYNACEFEVERIHELGYNTYASRLYRTGSSGPGA 143

Qy 163 -----RRYFVALNKDGTPRDGARSKRHQKFTHELPR 193

Db 144 QRPQAORPWYVSVNGKGRPRGFKTRRTQKSSLEFLPR 181

Search completed: October 21, 2002, 16:14:33
Job time : 13 secs


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Db 1 MAPLTVGAFGLGGLEGQVGSFHLPPAGERPPLLGERGALRGARGGSGVELAHL 60
Qy 61 HGILRRQLYCRGTGFHLQILPDGVSOGTQRDHSLSFGILFISVAVGLVSIKGVDSGLYL 120
Db 61 HGILRRQLYCRGTGFHLQILPDGVSOGTQRDHSLSFGILFISVAVGLVSIKGVDSGLYL 120
Qy 121 MNDKGLYGSKLTSECFRQEQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGR 180
Db 121 MNGKGLYGSKLTSECFRQEQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGR 180
Qy 181 SKRHQKFTFLPRPDPVPPELYKDLLMYT 211
Db 181 SKRHQKFTFLPRPDPVPPELYKDLLMYT 211
RESULT 2
Q9ESL9 ID Q9ESL9 PRELIMINARY; PRT; 212 AA.
AC Q9ESL9;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
GN FGF20.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Itoh N.;
RT "Mus musculus mRNA for FGF-20(FGF20).";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049218; BAB16406.1; -.
DR HSSP; P31371; IG82.
DR MGB; MGI:1891346; Fgf20.
DR InterPro; IPR002209; HBGF_FGF.
DR InterPro; IPR002348; ILI_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; ILIHGFG.
DR ProDom; PD000831; HBGF_FGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
SQ SEQUENCE 212 AA; 23659 MW; 174DBCE8915B69EF CRC64;

Query Match 95.6%; Score 1069; DB 11; Length 212;
Best Local Similarity 94.8%; Pred. No. 1.2e-97;
Matches 200; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MAPLAEVGGFLGGLEGQVGSFHLPPAGERPPLLGERSAERSARGGGAQLAHL 60
Db 1 MAPLTVGAFGLGGLEGQVGSFHLPPAGERPPLLGERGALRGARGGSGVELAHL 60
Qy 61 HGILRRQLYCRGTGFHLQILPDGVSOGTQRDHSLSFGILFISVAVGLVSIKGVDSGLYL 120
Db 61 HGILRRQLYCRGTGFHLQILPDGVSOGTQRDHSLSFGILFISVAVGLVSIKGVDSGLYL 120
Qy 121 MNDKGLYGSKLTSECFRQEQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGR 180
Db 121 MNDKGLYGSKLTSECFRQEQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGR 180
Qy 181 SKRHQKFTFLPRPDPVPPELYKDLLMYT 211
Db 181 SKRHQKFTFLPRPDPVPPELYKDLLMYT 211
RESULT 3
Q9PVY1 ID Q9PVY1 PRELIMINARY; PRT; 208 AA.
AC Q9PVY1;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
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DE XFGF-20.
GN XFGF-20.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99373151; Pubmed=10441498;
RA Kopa C., Adati N., Nakata K., Mikoshiba K., Furuhashi Y., Sato S.,
RA Tei H., Sakaki Y., Kurokawa T., Shikawa K., Yokoyama K.K.;
RT "Characterization of a novel member of the FGF family, XFGF-20, in
RL Xenopus laevis.";
RL Biochem. Biophys. Res. Commun. 261:756-765(1999).
DR EMBL; AB012615; BAA83474.1; -.
DR HSSP; P31371; IG82.
DR InterPro; IPR002209; HBGF_FGF.
DR InterPro; IPR002348; ILI_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; ILIHGFG.
DR ProDom; PD000831; HBGF_FGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
SQ SEQUENCE 208 AA; 23438 MW; 268881D36E757D4D CRC64;

Query Match 80.9%; Score 904.5; DB 13; Length 208;
Best Local Similarity 80.6%; Pred. No. 2.2e-81;
Matches 170; Conservative 19; Mismatches 19; Indels 3; Gaps 2;

Qy 1 MAPLAEVGGFLGGLEGQVGSFHLPPAGERPPLLGERSAERSARGGGAQLAHL 60
Db 1 MAPLADVTGFLGGYDALG-QVGSFHLPPAKDSPLLFNDFLAQSERLSRSAP--SDLSHL 57
Qy 61 HGILRRQLYCRGTGFHLQILPDGVSOGTQRDHSLSFGILFISVAVGLVSIKGVDSGLYL 120
Db 58 OGILRRQLYCRGTGFHLQILPDGVSOGTQRDHSLSFGILFISVAVGLVSIKGVDSGLYL 117
Qy 121 MNDKGLYGSKLTSECFRQEQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGR 180
Db 118 MNDKGLYGSKLTSECFRQEQFEENWNTYSSNIYKHGDSGRYFVALNKDGTPRDGT 177
Qy 181 SKRHQKFTFLPRPDPVPPELYKDLLMYT 211
Db 178 AKRHQKFTFLPRPDPPEKVPPELYKDLGYS 208

RESULT 4
Q95LL2 ID Q95LL2 PRELIMINARY; PRT; 208 AA.
AC Q95LL2;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE FIBROBLAST GROWTH FACTOR 9.
GN FGF9.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Paradis V., Silversides D.W.;
RT "Sus scrofa fgf9 cDNA.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY033825; AAK61609.2; -.
SQ SEQUENCE 208 AA; 23454 MW; 05FD0E2048CC05E5 CRC64;

Query Match 69.3%; Score 774.5; DB 6; Length 208;
Best Local Similarity 70.6%; Pred. No. 1.5e-68;
Matches 149; Conservative 24; Mismatches 29; Indels 9; Gaps 4;

Qy 1 MAPLAEVGGFLGGLEGQVGSFHLPPAGERPPLLGERSAERSARG--GFGAQL 57
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Db 1 MAPLGEVGNFYGVQDAV--PFGNVPVLPV--DSPVLLSDHLSQSE--AGGLPRGPVATDL 54
QY 58 AHLHGILRRQLCYRTGTHLQILPDGSGVQGTQDHSFLGILEFISVAVGLSVIRGVDGL 117
Db 55 DHLKGLLRRLQCYRTGTHLQILPDGSGVQGTQDHSFLGILEFISVAVGLSVIRGVDGL 114
QY 118 YLGMNDKGLYSEKLTSECIFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTGPRD 177
Db 115 YLGMNEKGLYSEKLTQECVFEQFEENWYNTYSSNIYKHVDIGRRFYVALNKDGTGPRE 174
QY 178 GASKRHQKFTHELPRVDPVPRVPELYKDLL 208
Db 175 GTRTKRHQKFTHELPRVDPVDPKVPYLYKDL 205

RESULT 5
Q9ERQ5 PRELIMINARY; PRT; 207 AA.
AC Q9ERQ5;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE FGF-16 PROTEIN.
GN FGF16.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Sontag D.P., Cattini P.A.;
RC TISSUE=HEART;
RT Cloning and biological function of FGF-16 in the heart.;
RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF292104; AAG29501.1; -.
DR HSSP; P31371; IG82.
DR MGD; MGI:1931627; Fgf16.
DR InterPro; IPR002209; HBGF_FGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; ILIHGFG.
DR ProDom; PD000831; HBGF_FGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
SQ SEQUENCE 207 AA; 23739 MW; E28004DED598A2C6 CRC64;

Query Match 63.3%; Score 707.5; DB 11; Length 207;
Best Local Similarity 63.2%; Pred. No. 6.3e-62;
Matches 134; Conservative 27; Mismatches 40; Indels 11; Gaps 4;

QY 4 LAEVGGFLGG---LEGIGQQVGSFHLPPAGERPPLLGERRSAAE--RSARGGPGAAQLA 58
Db 1 MAEVGGVFASLDWDLQGFSSSLGN---VPLADSPGFLNERLQIEGKLRGSP--TDFA 54
QY 59 HLHGILRRQLCYRTGTHLQILPDGSGVQGTQDHSFLGILEFISVAVGLSVIRGVDGL 118
Db 55 HLKGLLRRLQCYRTGTHLQILPDGSGVQGTQDHSFLGILEFISVAVGLSVIRGVDGL 114
QY 119 LGMNDKGLYSEKLTSECIFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTGPRD 178
Db 115 LGMNERGELYGSKLTRECVCFEQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTGPRD 174
QY 179 ARSKRHQKFTHELPRVDPVPRVPELYKDLLMY 210
Db 175 YRTRKHQKFTHELPRVDPVPSKLPSMSRDLRY 206

RESULT 6
Q9ESL8 PRELIMINARY; PRT; 207 AA.
AC Q9ESL8;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE FGF-4.
GN Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20112823; PubMed=10644718;
RT Munoiz-Sanjuan I., Smallwood P.M., Nathans J.;
RT Isoform Diversity among Fibroblast Growth Factor Homologous Factors
RT Is Generated by Alternative Promoter Usage and Differential
RT Splicing.;
RL J. Biol. Chem. 275:2589-2597(2000).
DR EMBL; AF199606; AAF31393.1; -.
DR HSSP; P31371; IG82.
DR InterPro; IPR002209; HBGF_FGF.
DR Pfam; PF00167; FGF; 1.

Query Match 62.7%; Score 700.5; DB 11; Length 207;
Best Local Similarity 62.7%; Pred. No. 3.1e-61;
Matches 133; Conservative 27; Mismatches 41; Indels 11; Gaps 4;

QY 4 LAEVGGFLGGLE---GLCQQVGSFHLPPAGERPPLLGERRSAAE--RSARGGPGAAQLA 58
Db 1 MAEVGGVFASLDWDLHGFFSSSLGN---VPLADSPGFLNERLQIEGKLRGSP--TDFA 54
QY 59 HLHGILRRQLCYRTGTHLQILPDGSGVQGTQDHSFLGILEFISVAVGLSVIRGVDGL 118
Db 55 HLKGLLRRLQCYRTGTHLQILPDGSGVQGTQDHSFLGILEFISVAVGLSVIRGVDGL 114
QY 119 LGMNDKGLYSEKLTSECIFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTGPRD 178
Db 115 LGMNERGELYGSKLTRECVCFEQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTGPRD 174
QY 179 ARSKRHQKFTHELPRVDPVPRVPELYKDLLMY 210
Db 175 YRTRKHQKFTHELPRVDPVPSKLPSMSRDLRY 206

RESULT 7
Q9IAI5 PRELIMINARY; PRT; 253 AA.
AC Q9IAI5;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE FIBROBLAST GROWTH FACTOR HOMOLOGOUS FACTOR 4 ISOFORM 1B.
GN FGF-4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20112823; PubMed=10644718;
RT Munoiz-Sanjuan I., Smallwood P.M., Nathans J.;
RT Isoform Diversity among Fibroblast Growth Factor Homologous Factors
RT Is Generated by Alternative Promoter Usage and Differential
RT Splicing.;
RL J. Biol. Chem. 275:2589-2597(2000).
DR EMBL; AF199606; AAF31393.1; -.
DR HSSP; P31371; IG82.
DR InterPro; IPR002209; HBGF_FGF.
DR Pfam; PF00167; FGF; 1.
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DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE FIBROBLAST GROWTH FACTOR 16.
GN FGF16.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Itoh N.;
RT "Mus musculus mRNA for FGF-16 (FGF16).";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049219; BAB16405.1; -.
DR HSSP; P31371; IG82.
DR MGD; MGI:1931627; Fgf16.
DR InterPro; IPR002209; HBGF_FGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; ILIHGFG.
DR ProDom; PD000831; HBGF_FGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
SQ SEQUENCE 207 AA; 23751 MW; 68BD03EBDAALD84E CRC64;

Query Match 62.7%; Score 700.5; DB 11; Length 207;
Best Local Similarity 62.7%; Pred. No. 3.1e-61;
Matches 133; Conservative 27; Mismatches 41; Indels 11; Gaps 4;

QY 4 LAEVGGFLGGLE---GLCQQVGSFHLPPAGERPPLLGERRSAAE--RSARGGPGAAQLA 58
Db 1 MAEVGGVFASLDWDLHGFFSSSLGN---VPLADSPGFLNERLQIEGKLRGSP--TDFA 54
QY 59 HLHGILRRQLCYRTGTHLQILPDGSGVQGTQDHSFLGILEFISVAVGLSVIRGVDGL 118
Db 55 HLKGLLRRLQCYRTGTHLQILPDGSGVQGTQDHSFLGILEFISVAVGLSVIRGVDGL 114
QY 119 LGMNDKGLYSEKLTSECIFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTGPRD 178
Db 115 LGMNERGELYGSKLTRECVCFEQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTGPRD 174
QY 179 ARSKRHQKFTHELPRVDPVPRVPELYKDLLMY 210
Db 175 YRTRKHQKFTHELPRVDPVPSKLPSMSRDLRY 206

RESULT 7
Q9IAI5 PRELIMINARY; PRT; 253 AA.
AC Q9IAI5;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE FIBROBLAST GROWTH FACTOR HOMOLOGOUS FACTOR 4 ISOFORM 1B.
GN FGF-4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20112823; PubMed=10644718;
RT Munoiz-Sanjuan I., Smallwood P.M., Nathans J.;
RT Isoform Diversity among Fibroblast Growth Factor Homologous Factors
RT Is Generated by Alternative Promoter Usage and Differential
RT Splicing.;
RL J. Biol. Chem. 275:2589-2597(2000).
DR EMBL; AF199606; AAF31393.1; -.
DR HSSP; P31371; IG82.
DR InterPro; IPR002209; HBGF_FGF.
DR Pfam; PF00167; FGF; 1.
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DR PRINTS: PR00262; IL1HBGF.
DR PRODOM: PD000831; HBGF_FGF; 1.
DR SMART: SM00442; FGF; 1.
DR PROSITE: PS00247; HBGF_FGF; 1.
SQ SEQUENCE 253 AA; 28640 MW; 5AEFD9F9D6E74305 CRC64;

Query Match 28.3%; Score 316.5; DB 13; Length 253;
Best Local Similarity 38.4%; Pred. No. 3.6e-23;
Matches 71; Conservative 34; Mismatches 61; Indels 19; Gaps 4;

QY 22 GSHFLLPAGERPPLLGGERRSAARGPGAAQLAHLHLGILRRRLQYCRGTFHQLILP 81
DB 50 GSHMLQCLCG-----KSLKKKNKQTD-----QLKGIVTR--LYCRQGYLQMH 92

QY 82 DGSVOGTRODHSFLGILFISVAVGLVIRGVDGSLYLGMDKGLYSEKLTSECFIRE 141
DB 93 DGSGLGTDKSSNSLFLNLPVGLRVVAIQGYKTGLYIALNNEGFLYTSFLTPCKE 152

QY 142 QFEENWNTYSSNIYKHGDTGRYFVALNKDGTPRDGARSRKHOKFTHFLPRVPDPE--R 199
DB 153 SVFENYVIYSSMLYRQESGRAWFLGLNKGQVMKGNRVKTKPAAHFLPKPLEVAMYR 212

QY 200 VPELY 204
DB 213 EPSLH 217

RESULT 8
Q9IAI6 PRELIMINARY; PRT; 237 AA.
AC Q9IAI6;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE FIBROBLAST GROWTH FACTOR HOMOLOGOUS FACTOR 4 ISOFORM 1A
DE (FRAGMENT).
GN FHF-4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112823; PubMed=10644718;
RA Munoz-Sanjuan I., Smallwood P.M., Nathans J.;
RT "Isoform Diversity among Fibroblast Growth Factor Homologous Factors
RT Is Generated by Alternative Promoter Usage and Differential
RT Splicing.";
RL J. Biol. Chem. 275:2589-2597(2000).
DR EMBL; AF199605; AAF31392.1; -.
DR HSSP; P31371; IG82.
DR InterPro: IPR002209; HBGF_FGF.
DR ProDom: PD002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRODOM: PD000831; HBGF_FGF; 1.
DR SMART; SM00442; FGF; 1_HBGF.
DR PROSITE; PS00247; HBGF_FGF; 1.
FT NON_TER
SQ SEQUENCE 237 AA; 26816 MW; FL3076736548BB22 CRC64;

Query Match 28.3%; Score 316; DB 13; Length 237;
Best Local Similarity 43.5%; Pred. No. 3.7e-23;
Matches 64; Conservative 31; Mismatches 48; Indels 4; Gaps 2;

QY 60 LHGILRRRLQYCRGTFHQLILPDGSGVGTQRDHSFLGILEFISVAVGLVIRGVDGSLYL 119
DB 57 LKGIVTR--LYCRQGYLQMHDPGSLDGTDDSSNSTLFLNLPVGLRVVAIQGVKTGLYI 114

QY 120 GMNDKGLYSEKLTSCIFRQFEENWNTYSSNIYKHGDTGRYFVALNKDGTPRDGA 179
DB 115 ALNNEGFLYTSFLTPCKFKESVFENYVIYSSMLYRQESGRAWFLGLNKGQVMKGN 174
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QY 180 RSKRHQKFTHELPRVPDPE--RVPELY 204
DB 175 RVKTKPAAHFLPKPLEVAMYREPSLH 201

RESULT 9
O89096 PRELIMINARY; PRT; 252 AA.
AC O89096;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE FHF-4B.
GN FGF14.
OS Rattus norvegicus (Rat), and
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116, 10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=98267141; PubMed=9602045;
RA Yamamoto S., Mikami T., Ohbayashi N., Ohta M., Itoh N.;
RT "Structure and expression of a novel isoform of mouse FGF homologous
RT factor (FHF)-4.";
RL Biochim. Biophys. Acta 1398:38-41(1998).
DR EMBL; AB008908; BAA31544.1; -.
DR EMBL; AB008907; BAA31543.1; -.
DR HSSP; P31371; IG82.
DR MGD; MGI:109189; Fgf14.
DR InterPro: IPR002209; HBGF_FGF.
DR Pfam; PF00167; FGF; 1.
DR PRODOM: PD000831; HBGF_FGF; 1.
DR SMART; SM00442; FGF; 1_HBGF.
DR PROSITE; PS00247; HBGF_FGF; 1.
SQ SEQUENCE 252 AA; 28364 MW; 281781EBA63AB44 CRC64;

Query Match 27.9%; Score 312; DB 11; Length 252;
Best Local Similarity 42.9%; Pred. No. 9.9e-23;
Matches 63; Conservative 31; Mismatches 49; Indels 4; Gaps 2;

QY 60 LHGILRRRLQYCRGTFHQLILPDGSGVGTQRDHSFLGILEFISVAVGLVIRGVDGSLYL 119
DB 73 LKGIVTR--LYCRQGYLQMHDPGSLDGTDDSSNSTLFLNLPVGLRVVAIQGVKTGLYI 130

QY 120 GMNDKGLYSEKLTSCIFRQFEENWNTYSSNIYKHGDTGRYFVALNKDGTPRDGA 179
DB 131 AMNGEGYLYPSELTPCKFKESVFENYVIYSSMLYRQESGRAWFLGLNKGQVMKGN 190

QY 180 RSKRHQKFTHELPRVPDPE--RVPELY 204
DB 191 RVKTKPAAHFLPKPLEVAMYREPSLH 217

RESULT 10
Q95K97 PRELIMINARY; PRT; 208 AA.
AC Q95K97;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE HYPOTHETICAL 23.5 KDA PROTEIN.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MEDULLA OBLOGATA;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
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[illegible]

Db 148 NDCKLXERIEGNYTYASFENQH--NGRQWYVALNGKGAPRGOKTRKNTSAHFLEPMV 205

QY 195 V 195

Db 206 V 206

Search completed: October 21, 2002, 16:15:09
Job time : 30 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: October 21, 2002, 16:15:16 ; Search time 31 seconds
(without alignments)
756.018 Million cell updates/sec

Title: US-09-817-814-2

Perfect score: 211

Sequence: 1 MAPLAEVGGFLGLEGLGQQ.....PRPVDPERVPELYKDLLMYT 211

Scoring table: OLIGO

Gapop 60.0 , Capext 60.0

Searched: 747574 seqs, 11107396 residues

Word size: 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database: A_Geneseq_032802.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	211	100.0	211	AA18635	Amino acid sequenc
2	211	100.0	211	AAU09931	Human fibroblast g
3	211	100.0	211	AAU09931	Human fibroblast g
4	211	100.0	211	AAU02081	Human fibroblast g
5	211	100.0	211	AAU02081	Human fibroblast g
6	85	40.3	212	AAU02081	Rat fibroblast gro
7	19	9.0	142	AAU02081	Glia activating fa
8	19	9.0	159	AAU02081	Glia activating fa
9	19	9.0	160	AAU02081	Glia activating fa
10	19	9.0	175	AAU02081	Glia activating fa
11	19	9.0	176	AAU02081	Glia activating fa

12	19	9.0	177	13	AAU02081	Glia activating fa
13	19	9.0	178	13	AAU02081	Glia activating fa
14	19	9.0	205	13	AAU02081	Glia activating fa
15	19	9.0	205	15	AAU02081	Glia activating fa
16	19	9.0	206	13	AAU02081	Glia activating fa
17	19	9.0	206	13	AAU02081	Glia activating fa
18	19	9.0	206	15	AAU02081	Glia activating fa
19	19	9.0	207	15	AAU02081	Glia activating fa
20	19	9.0	208	13	AAU02081	Glia activating fa
21	19	9.0	208	13	AAU02081	Glia activating fa
22	19	9.0	208	15	AAU02081	Glia activating fa
23	19	9.0	208	16	AAU02081	Glia activating fa
24	19	9.0	208	16	AAU02081	Glia activating fa
25	19	9.0	208	18	AAU02081	Glia activating fa
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28	19	9.0	208	21	AAU02081	Glia activating fa
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31	19	9.0	208	21	AAU02081	Glia activating fa
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47	16	7.6	173	21	AAU02081	Glia activating fa
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52	16	7.6	173	21	AAU02081	Glia activating fa
53	11	5.2	61	17	AAU02081	Glia activating fa
54	10	4.7	14	18	AAU02081	Glia activating fa
55	9	4.3	27	16	AAU02081	Glia activating fa
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78	7	3.3	124	21	AAU02081	Glia activating fa
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85	7	3.3	145	20	AAV37604	Protein which is s	158	7	3.3	711	20	AAW86021	Human lactoferrin
86	7	3.3	158	22	AAB93271	Human protein sequ	159	7	3.3	711	21	AAW86021	Amino acid sequenc
87	7	3.3	174	22	AAW40400	Human polypeptide	160	7	3.3	711	21	AAW86021	Human lactoferrin
88	7	3.3	181	19	AAW39181	Human PKD1 protein	161	7	3.3	711	21	AAW77578	Human lactoferrin
89	7	3.3	189	22	AAW42186	Human polypeptide	162	7	3.3	711	22	AAW42186	Chronic hepatitis
90	7	3.3	201	19	AAW39182	Human PKD1 protein	163	7	3.3	711	22	AAW42186	Human lactoferrin
91	7	3.3	217	22	ABG23027	Novel human diagno	164	7	3.3	711	22	AAW36843	Human lactoferrin
92	7	3.3	224	21	AAW44861	Human taste cell s	165	7	3.3	732	21	AAW44861	Arabidopsis thalia
93	7	3.3	224	21	AAW44861	Human taste cell s	166	7	3.3	732	21	AAW44861	Arabidopsis thalia
94	7	3.3	233	21	AAW30097	Arabidopsis thalia	167	7	3.3	732	21	AAW44861	Arabidopsis thalia
95	7	3.3	236	21	AAW30096	Arabidopsis thalia	168	7	3.3	758	21	AAW41293	Human ORFX ORF1057
96	7	3.3	239	21	AAW30095	Arabidopsis thalia	169	7	3.3	758	21	AAW41293	Arabidopsis thalia
97	7	3.3	244	21	AAW30095	Arabidopsis thalia	170	7	3.3	763	21	AAW42390	Arabidopsis thalia
98	7	3.3	258	21	AAW47700	Arabidopsis thalia	171	7	3.3	772	21	AAW42390	Arabidopsis thalia
99	7	3.3	260	20	AAW37417	Amino acid sequenc	172	7	3.3	783	22	ABW1349	Drosophila melanog
100	7	3.3	262	22	AAW32123	Arabidopsis thalia	173	7	3.3	853	21	AAW46917	Large subunit of p
101	7	3.3	266	22	ABG05763	Novel human diagno	174	7	3.3	1003	22	ABG23021	Novel human diagno
102	7	3.3	282	19	AAW72018	HSV-2 strain SB5 C	175	7	3.3	1025	16	AAW70126	Serum opacity fact
103	7	3.3	323	19	AAW64461	Human secreted pro	176	7	3.3	1025	16	AAW70126	Novel human diagno
104	7	3.3	323	22	AAW93897	Human protein sequ	177	7	3.3	1028	22	ABG15393	Drosophila melanog
105	7	3.3	357	19	AAW72208	HSV-2 strain SB5 C	178	7	3.3	1058	22	ABW62096	Novel human diagno
106	7	3.3	364	21	AAW35260	HSV-2 strain SB5 C	179	7	3.3	1120	22	ABW68196	C glutamic prote
107	7	3.3	373	22	AAW40200	Human polypeptide	180	7	3.3	1233	22	AAW90558	Novel human diagno
108	7	3.3	381	21	AAW35259	Zea mays protein f	181	7	3.3	1235	22	ABG17056	Novel human diagno
109	7	3.3	384	21	AAW71056	Zea mays protein f	182	7	3.3	1270	22	ABG17056	Novel human diagno
110	7	3.3	384	22	AAW40198	Human membrane tra	183	7	3.3	1355	22	ABW63317	Drosophila melanog
111	7	3.3	384	22	AAW40198	Human polypeptide	184	7	3.3	1355	22	ABW63317	Novel human diagno
112	7	3.3	388	21	AAW35258	Zea mays protein f	185	7	3.3	1614	16	AAW75917	Novel human diagno
113	7	3.3	391	22	AAW67472	Amino acid sequenc	186	7	3.3	1614	16	AAW75917	Novel human diagno
114	7	3.3	414	22	AAW78215	Human MAP kinase i	187	7	3.3	3313	22	AAW30134	Polycystic kidney
115	7	3.3	424	18	AAW23818	LEAFY gene product	188	7	3.3	3390	22	AAW07990	Wild-type, virulen
116	7	3.3	424	19	AAW45512	Arabidopsis floral	189	7	3.3	3390	22	AAW07990	Attenuated, vaccin
117	7	3.3	424	19	AAW43332	Arabidopsis floral	190	7	3.3	3390	22	AAW07990	Novel human diagno
118	7	3.3	424	21	AAW39138	Amino acid sequenc	191	7	3.3	4292	22	ABG17060	Polycystic kidney
119	7	3.3	424	21	AAW19248	A. thaliana LFY pr	192	7	3.3	4302	17	AAW00870	Human PKD1 polypep
120	7	3.3	424	21	AAW75557	Novel human secret	193	7	3.3	4302	19	AAW33396	Human PKD1 polypep
121	7	3.3	424	21	AAW78886	Novel human secret	194	7	3.3	4302	21	AAW27919	Human polycystin
122	7	3.3	458	22	AAU31109	Novel human neopla	195	7	3.3	4303	17	AAW90302	Polycystic kidney
123	7	3.3	469	22	AAW42077	Drosophila melanog	196	7	3.3	4303	17	AAW90302	Polycystic kidney
124	7	3.3	567	22	AAU21696	Human protein sequ	197	7	3.3	4339	16	AAW75916	Polycystic kidney
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126	7	3.3	637	22	AAW94689	Novel human diagno	199	7	3.3	4725	22	ABG23837	Novel human diagno
127	7	3.3	643	22	ABW11071	Novel human diagno	200	7	3.3	4725	22	ABG17057	Novel human diagno
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129	7	3.3	678	22	ABW58061	Mutant human lacto	202	6	2.8	6	22	AAU02085	Rat fibroblast gro
130	7	3.3	687	22	AAW71183	Human lactoferrin	203	6	2.8	6	22	AAU02087	Rat fibroblast gro
131	7	3.3	687	22	AAW77911	Mutant human lacto	204	6	2.8	6	22	AAU02088	Rat fibroblast gro
132	7	3.3	688	19	AAW71182	Human lactoferrin	205	6	2.8	6	22	AAU02088	Flavoprotein Epid
133	7	3.3	688	22	AAW77910	Mutant human lacto	206	6	2.8	8	20	AAW43458	Procollagen alpha
134	7	3.3	689	22	AAW71181	Mutant human lacto	207	6	2.8	10	22	AAW93400	Amino acid sequenc
135	7	3.3	689	22	AAW77909	Mutant human lacto	208	6	2.8	10	22	AAW93400	Vaccine related MH
136	7	3.3	690	22	AAW71180	Mutant human lacto	209	6	2.8	11	19	AAW59848	Sequence of beta-D
137	7	3.3	690	22	AAW77908	Human lactoferrin	210	6	2.8	14	22	AAW98915	Amino acid sequenc
138	7	3.3	692	21	AAW58733	Human lactoferrin	211	6	2.8	15	19	AAW59853	HLA-A2-binding HIV
139	7	3.3	692	22	AAW77906	Human lactoferrin	212	6	2.8	15	21	AAW66451	Peptide #4792 enco
140	7	3.3	692	22	AAW97382	Lactoferrin protel	213	6	2.8	17	22	AAW0520	Peptide #4641 enco
141	7	3.3	693	16	AAW85146	Human lactoferrin	214	6	2.8	17	22	AAW0520	Peptide #11780 enc
142	7	3.3	705	13	AAW22423	Human lactoferrin	215	6	2.8	25	22	ABW44274	Tryptic peptide fr
143	7	3.3	705	20	AAW31152	Human lactoferrin	216	6	2.8	25	22	AAW05959	Human secreted pro
144	7	3.3	708	20	AAW22424	Human lactoferrin	217	6	2.8	26	22	ABW50711	Human colon cancer
145	7	3.3	708	20	AAW31153	Human lactoferrin	218	6	2.8	26	22	ABW50711	pl8 of nef peptide
146	7	3.3	709	15	AAW45199	Human lactoferrin	219	6	2.8	29	22	AAW77091	Human polypeptide
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148	7	3.3	709	18	AAW21695	Human lactoferrin	221	6	2.8	32	22	AAW07983	Human polypeptide
149	7	3.3	709	18	AAW3879	Human lactoferrin	222	6	2.8	33	10	AAW92272	Human colon cancer
150	7	3.3	709	21	AAW03830	Human lactoferrin	223	6	2.8	33	22	AAW75761	Human polypeptide
151	7	3.3	709	21	AAW77577	Protein encoded by	224	6	2.8	34	22	AAW09532	Human polypeptide
152	7	3.3	709	22	AAW36842	Human lactoferrin	225	6	2.8	34	22	AAW09532	Supernatant pepti
153	7	3.3	711	11	AAW08033	Lactoferrin, Homo	226	6	2.8	40	16	AAW74070	HIV Negative facti
154	7	3.3	711	14	AAW43653	Human lactoferrin	227	6	2.8	40	20	AAW39989	Human secreted pro
155	7	3.3	711	17	AAW09342	Human lactoferrin	228	6	2.8	41	21	AAW91544	Cytomegalovirus la
156	7	3.3	711	19	AAW57317	Human lactoferrin	229	6	2.8	42	18	AAW06501	
157	7	3.3	711	19	AAW53880	Bovine alphaS1-cas	230	6	2.8	42	18	AAW06501	

231	6	2.8	43	22	ABB39963	Peptide #7469 enco	304	6	2.8	80	21	ABG04361	Arabidopsis thalia
232	6	2.8	43	22	ABR24497	Protein #6496 enco	305	6	2.8	80	22	ABG17801	Novel human thalia
233	6	2.8	43	22	RAM60708	Human brain expres	306	6	2.8	80	22	ABH11126	Human secreted pro
234	6	2.8	43	22	RAM73581	Human bone marrow	307	6	2.8	82	20	AAI12445	Human 5' EST secre
235	6	2.8	43	22	AAAM3583	Peptide #7620 enco	308	6	2.8	83	13	AAAR28992	Encoded by human G
236	6	2.8	46	14	AAAR42695	p14 of nef peptide	309	6	2.8	83	16	AAAR94760	nef CTL epitope d
237	6	2.8	47	20	AAAY12851	Human 5' EST secre	310	6	2.8	83	22	ABH17990	Human nervous syst
238	6	2.8	48	10	AAAP92268	Peptide pF14 from	311	6	2.8	83	22	AAAR88619	Human immune/haema
239	6	2.8	48	22	ABBA1227	Peptide #8733 enco	312	6	2.8	83	22	AAAR98916	HIV Nef-1 CTL epit
240	6	2.8	49	22	ABR25233	Protein #7232 enco	313	6	2.8	84	22	ABG12684	Novel human thalia
241	6	2.8	49	22	AAAM62091	Human brain expres	314	6	2.8	86	22	AAAR83146	Novel human thalia
242	6	2.8	49	22	AAAM74893	Human bone marrow	315	6	2.8	87	20	AAAY60427	Human immune/haema
243	6	2.8	49	22	AAAM35009	Peptide #9046 enco	316	6	2.8	88	22	AAAG75581	Human normal bladd
244	6	2.8	52	22	AAAU43770	Propionibacterium	317	6	2.8	88	22	AAAG66908	Human colon cancer
245	6	2.8	54	22	AAAU49248	Propionibacterium	318	6	2.8	89	22	AAAG65512	Propionibacterium
246	6	2.8	55	22	AAAU43205	Propionibacterium	319	6	2.8	89	22	ABG26496	Novel human thalia
247	6	2.8	55	22	ABR30939	Peptide #3590 enco	320	6	2.8	90	22	AAU56667	Propionibacterium
248	6	2.8	55	22	ABR36129	Peptide #3635 enco	321	6	2.8	91	22	AAU59395	Propionibacterium
249	6	2.8	55	22	ABR21514	Protein #3513 enco	322	6	2.8	91	22	AAU59395	Propionibacterium
250	6	2.8	55	22	AAU21172	Human novel foetal	323	6	2.8	93	21	AAAG04360	Arabidopsis thalia
251	6	2.8	55	22	AAAM56912	Human brain expres	324	6	2.8	96	21	AAAG27221	zea mays protein f
252	6	2.8	55	22	AAAM69300	Human novel foetal	325	6	2.8	96	21	AAAG27221	Propionibacterium
253	6	2.8	55	22	AAAM17125	Peptide #3559 enco	326	6	2.8	96	22	AAU57327	Propionibacterium
254	6	2.8	55	22	AAAM29619	Peptide #3656 enco	327	6	2.8	96	22	AAAG67744	Amino acid sequenc
255	6	2.8	56	22	AAU58509	Propionibacterium	328	6	2.8	96	22	AAO05429	Human polypeptide
256	6	2.8	56	22	ABG01841	Novel human thalia	329	6	2.8	97	21	AAAG58758	Arabidopsis thalia
257	6	2.8	56	22	ABG01842	Novel human thalia	330	6	2.8	97	22	AAU46317	Propionibacterium
258	6	2.8	57	22	AAAR92434	Miscellaneous pept	331	6	2.8	99	21	AAAG16013	Arabidopsis thalia
259	6	2.8	58	22	AAU60226	Propionibacterium	332	6	2.8	99	22	AAAG63913	Propionibacterium
260	6	2.8	60	22	AAAE00643	Human fibroblast g	333	6	2.8	100	21	AAAB59093	Breast and ovarian
261	6	2.8	61	20	AAAY12082	Human 5' EST secre	334	6	2.8	100	21	AAAB41525	Human ORFX ORF1289
262	6	2.8	61	22	ABH11863	Human cathepsin L	335	6	2.8	102	21	AAAG16012	Arabidopsis thalia
263	6	2.8	62	20	AAAY11669	Human 5' EST secre	336	6	2.8	102	22	ABH16216	Human nervous syst
264	6	2.8	62	22	AAU44829	Propionibacterium	337	6	2.8	103	21	AAAG13823	Arabidopsis thalia
265	6	2.8	64	22	AAAG61989	Propionibacterium	338	6	2.8	103	22	AAAG8927	Human immune/haema
266	6	2.8	64	22	ABR34775	Peptide #2246 enco	339	6	2.8	103	22	AAAG66011	Human secreted pro
267	6	2.8	64	22	ABR34775	Peptide #2281 enco	340	6	2.8	104	22	AAU25689	G protein-coupled
268	6	2.8	64	22	ABR20190	Protein #2189 enco	341	6	2.8	105	22	AAO10255	Human polypeptide
269	6	2.8	64	22	AAAM55577	Human brain expres	342	6	2.8	106	14	AAAR36386	Urease beta subuni
270	6	2.8	64	22	AAAM65652	Human brain expres	343	6	2.8	106	22	AAAR92785	Human digestive sy
271	6	2.8	64	22	AAAM67959	Human bone marrow	344	6	2.8	106	22	AAAR94685	Human protein sequ
272	6	2.8	64	22	AAAM78268	Human bone marrow	345	6	2.8	108	21	AAAG16011	Arabidopsis thalia
273	6	2.8	64	22	AAAM15778	Peptide #2212 enco	346	6	2.8	108	21	AAAG58757	Arabidopsis thalia
274	6	2.8	64	22	AAAM28288	Peptide #2325 enco	347	6	2.8	109	21	AAAG24511	Arabidopsis thalia
275	6	2.8	64	22	AAAM03513	Peptide #2195 enco	348	6	2.8	109	22	ABG24079	Novel human thalia
276	6	2.8	66	21	AAAG04362	Arabidopsis thalia	349	6	2.8	110	21	AAAG24510	Arabidopsis thalia
277	6	2.8	66	22	AAAM23882	Human EST encoded	350	6	2.8	110	22	ABH50710	Human secreted pro
278	6	2.8	68	17	AAAR81547	Promersacidin lant	351	6	2.8	110	22	AAAM4713	Human immune/haema
279	6	2.8	68	22	AAAM80077	Human protein SEQ	352	6	2.8	110	22	AAAM25787	Human protein sequ
280	6	2.8	70	21	AAAB18677	Peptide fragment f	353	6	2.8	111	22	AAAG1511	Propionibacterium
281	6	2.8	70	21	AAAB18679	Mutant peptide der	354	6	2.8	111	22	AAAG81511	S. epidermidis ope
282	6	2.8	70	21	AAAB18680	Mutant peptide der	355	6	2.8	111	22	AAAM50300	Human fibroblast g
283	6	2.8	70	21	AAAB18681	Mutant peptide der	356	6	2.8	112	22	AAAM83853	Human immune/haema
284	6	2.8	70	21	AAAB18682	Mutant peptide der	357	6	2.8	112	20	AAAY14141	zea mays SCLBR pro
285	6	2.8	70	21	AAAB18683	Mutant peptide der	358	6	2.8	114	21	AAAG13822	Arabidopsis thalia
286	6	2.8	70	21	AAAB18684	Mutant peptide der	359	6	2.8	114	21	AAAG17801	Propionibacterium
287	6	2.8	70	21	AAAB18685	Mutant peptide der	360	6	2.8	115	22	AAU53166	Propionibacterium
288	6	2.8	70	21	AAAB18686	Mutant peptide der	361	6	2.8	117	22	AAAG24509	Propionibacterium
289	6	2.8	70	21	AAAB18688	Mutant peptide der	362	6	2.8	118	21	AAAG24509	Arabidopsis thalia
290	6	2.8	70	21	AAAB18689	Mutant peptide der	363	6	2.8	119	22	AAAM41833	Human polypeptide
291	6	2.8	70	21	AAAB18690	Mutant peptide der	364	6	2.8	120	21	AAAB43106	Human ORFX ORF2870
292	6	2.8	70	21	AAAB18691	Mutant peptide der	365	6	2.8	120	22	AAU32167	Novel human secret
293	6	2.8	70	21	AAAB18692	Mutant peptide der	366	6	2.8	121	19	AAAR23892	Murine fibroblast
294	6	2.8	70	21	AAAY91690	Human secreted pro	367	6	2.8	121	21	AAAY97888	Rat fibroblast gro
295	6	2.8	70	22	ABG25882	Novel human thalia	368	6	2.8	121	22	AAAM61270	Human brain expres
296	6	2.8	71	20	AAAY05629	HIV-1 group O isol	369	6	2.8	121	22	AAAM73993	Human bone marrow
297	6	2.8	73	22	AAU633369	Propionibacterium	370	6	2.8	122	22	AAU17273	Novel signal trans
298	6	2.8	73	22	AAU63962	Propionibacterium	371	6	2.8	122	16	AAAR75407	Protein encoded by
299	6	2.8	75	20	AAAY48581	Human breast tumou	372	6	2.8	122	20	AAAY36111	HIV-3 strain AMT70
300	6	2.8	75	22	AAU54326	Propionibacterium	373	6	2.8	122	22	ABG22209	Extended human sec
301	6	2.8	76	22	ABH15813	Human nervous syst	374	6	2.8	123	19	AAAR23891	Novel human thalia
302	6	2.8	78	22	AAU41559	Propionibacterium	375	6	2.8	123	22	AAAR80395	Human fibroblast g
303	6	2.8	79	22	AAU47735	Propionibacterium	376	6	2.8	123	22	AAAB86000	Secreted protein e
										125	22	ABG27466	Amino acid sequenc
										125	22	ABG27466	Novel human thalia

377	6	2.8	125	22	AAG73819	Human colon cancer	450	6	2.8	177	12	AAR12787	Non-glycosylated f
378	6	2.8	126	22	AAM90373	Human immune/haema	451	6	2.8	177	21	AAG08237	Arabidopsis thalia
379	6	2.8	127	22	AAU43595	Propionibacterium	452	6	2.8	178	21	AAB41654	Human ORFX ORF1418
380	6	2.8	127	22	AAU54171	Propionibacterium	453	6	2.8	178	21	AAG08236	Arabidopsis thalia
381	6	2.8	127	22	AAU65852	Propionibacterium	454	6	2.8	178	22	AAU20429	Human secreted pro
382	6	2.8	127	22	AAU93585	Human polypeptide,	455	6	2.8	182	22	ABG68284	Drosophila melanog
383	6	2.8	128	21	AAG01030	Human secreted pro	456	6	2.8	182	22	AAU39281	Human polypeptide
384	6	2.8	128	21	AAY95014	Human secreted pro	457	6	2.8	182	22	AAU19434	Human diagnostic a
385	6	2.8	129	10	AAU91577	Sequence of electr	458	6	2.8	183	22	ABU12276	Human secretory pr
386	6	2.8	129	21	AAU42396	Human ORFX ORF2160	459	6	2.8	183	22	AAU39354	Human protein sequ
387	6	2.8	129	21	AAY51200	Human SCF7 protein	460	6	2.8	185	22	AAU18526	Human cytoskeletal
388	6	2.8	129	22	AAM00853	Human bone marrow	461	6	2.8	186	22	ABG10962	Novel human diago
389	6	2.8	131	22	ABG64217	Drosophila melanog	462	6	2.8	186	22	ABG87419	Human gene 3 encod
390	6	2.8	131	22	ABG07046	Novel human diago	463	6	2.8	187	21	AAU42918	Human ORFX ORF2682
391	6	2.8	132	21	AAU81275	Mature M13 coat pr	464	6	2.8	189	21	AAU16513	Arabidopsis thalia
392	6	2.8	133	21	AAU12936	Arabidopsis thalia	465	6	2.8	189	22	AAU42341	Propionibacterium
393	6	2.8	133	21	AAU53254	Arabidopsis thalia	466	6	2.8	189	22	ABG25347	Novel human diago
394	6	2.8	133	21	AAU57056	Arabidopsis thalia	467	6	2.8	191	22	AAU39671	Human polypeptide
395	6	2.8	133	22	AAU39192	Propionibacterium	468	6	2.8	191	22	AAU39671	Human protein sequ
396	6	2.8	133	22	AAU00811	Human polypeptide	469	6	2.8	192	22	AAU39279	Human polypeptide
397	6	2.8	133	22	AAU52450	Mycobacterium tube	470	6	2.8	195	22	AAU59583	Human protein sequ
398	6	2.8	134	21	AAU27219	Zea mays protein f	471	6	2.8	196	21	AAU86141	S. pneumoniae deri
399	6	2.8	134	22	AAU60483	Propionibacterium	472	6	2.8	196	22	ABG24087	Novel human diago
400	6	2.8	136	22	AAU36591	Staphylococcus aur	473	6	2.8	196	22	AAU25435	Human protein sequ
401	6	2.8	137	21	AAU70555	Arabidopsis thalia	474	6	2.8	196	22	ABG10731	Novel human diago
402	6	2.8	137	22	ABG10729	Novel human diago	475	6	2.8	198	16	AAU80781	Fibroblast growth
403	6	2.8	138	18	AAU20425	H. pylori inner me	476	6	2.8	198	16	AAU70826	FGF-6. Homo sapie
404	6	2.8	138	18	AAU24659	H. pylori inner me	477	6	2.8	198	19	AAU75716	Fibroblast growth
405	6	2.8	138	20	AAU12378	Human 5' EST seque	478	6	2.8	198	19	AAU53032	Fibroblast growth
406	6	2.8	139	22	ABU10252	Human cDNA SEQ ID	479	6	2.8	198	21	AAU10295	Fibroblast growth
407	6	2.8	140	15	AAU54339	Truncated K-FGF.	480	6	2.8	198	21	AAU90415	FGF-6, SEQ ID NO:1
408	6	2.8	141	22	AAU63931	Propionibacterium	481	6	2.8	198	21	AAU32338	Human fibroblast g
409	6	2.8	141	22	AAU03095	Human polypeptide	482	6	2.8	199	22	AAU61659	FGF6 protein. Hom
410	6	2.8	142	21	AAU87346	Human signal pepti	483	6	2.8	199	22	AAU60327	Propionibacterium
411	6	2.8	142	22	AAU07110	Human gene 6 encod	484	6	2.8	199	22	ABG05956	Novel human diago
412	6	2.8	143	22	AAU25369	Human protein sequ	485	6	2.8	199	22	ABG23314	S. epidermidis ope
413	6	2.8	146	15	AAU58554	Mutant heparin-bin	486	6	2.8	201	21	AAU74633	Neisseria gonorrhoe
414	6	2.8	146	21	AAU53236	Human colon cancer	487	6	2.8	201	22	AAU39670	Human polypeptide
415	6	2.8	146	22	AAU59151	Propionibacterium	488	6	2.8	202	22	AAU09290	Fibroblast growth
416	6	2.8	147	12	AAU11464	Hst-1 mutain N27.	489	6	2.8	202	22	AAU85833	Murine fibroblast
417	6	2.8	147	22	AAU74930	Human colon cancer	490	6	2.8	202	22	AAU45801	Rat kPGF protein.
418	6	2.8	148	13	AAU21608	Heparin binding se	491	6	2.8	203	22	AAU92720	C. glutamicum prote
419	6	2.8	148	15	AAU48559	Sequence of mutain	492	6	2.8	204	22	AAU29778	Novel human secret
420	6	2.8	150	21	AAU56957	Human prostate can	493	6	2.8	205	21	AAU87851	Human EGF-4 protei
421	6	2.8	152	21	AAU57054	Arabidopsis thalia	494	6	2.8	206	7	AAU61515	Sequence of E' pro
422	6	2.8	153	21	AAU41043	Human ORFX ORF807	495	6	2.8	206	9	AAU81859	Sequence encoded b
423	6	2.8	153	22	AAU31759	Novel human secret	496	6	2.8	206	14	AAU38893	Nef protein of HIV
424	6	2.8	154	15	AAU56458	Murine protein tyr	497	6	2.8	206	15	AAU48557	Sequence of hepari
425	6	2.8	156	22	AAU42675	Propionibacterium	498	6	2.8	206	16	AAU80779	Fibroblast growth
426	6	2.8	157	22	AAU81032	Human haematologic	499	6	2.8	206	16	AAU70825	FGF-4. Homo sapie
427	6	2.8	157	22	AAU81503	Human secreted pro	500	6	2.8	206	19	AAU75714	Fibroblast growth
428	6	2.8	159	21	AAU01797	Human secreted pro	501	6	2.8	206	19	AAU53030	Fibroblast growth
429	6	2.8	159	22	AAU76010	Human colon cancer	502	6	2.8	206	20	AAU90179	HTLV-III E' protei
430	6	2.8	160	20	AAU82488	Ehrlichia sp. E74.	503	6	2.8	206	20	AAU89326	HIV-1 nef protein
431	6	2.8	161	13	AAU24301	Glycopeptide resis	504	6	2.8	206	21	AAU69361	HIV-1 non-subtype
432	6	2.8	161	22	AAU49164	Propionibacterium	505	6	2.8	206	21	AAU69363	HIV-1 non-subtype
433	6	2.8	163	22	AAU96132	Putative 3-isoprop	506	6	2.8	206	21	AAU10294	Fibroblast growth
434	6	2.8	163	22	AAU18031	Human immunoglobul	507	6	2.8	206	21	AAU10054	HIV-1 nef proteoin.
435	6	2.8	163	22	AAU20397	Human secreted pro	508	6	2.8	206	21	AAU90413	FGF-4, SEQ ID NO:1
436	6	2.8	168	21	AAU28962	Arabidopsis thalia	509	6	2.8	206	21	AAU32336	Human fibroblast g
437	6	2.8	169	22	AAU36376	Human gastric canc	510	6	2.8	206	21	AAU50795	Human NEF proteoin/
438	6	2.8	170	22	ABG19395	Novel human diago	511	6	2.8	206	22	AAU65650	Human fibroblast g
439	6	2.8	171	15	AAU58553	Mutant heparin-bin	512	6	2.8	206	22	AAU5815	Human fibroblast g
440	6	2.8	171	22	ABG19376	Novel human diago	513	6	2.8	206	22	AAU04403	FGF4 protein. Hom
441	6	2.8	175	13	AAU21607	Heparin binding se	514	6	2.8	206	22	AAU61658	Human FGF-4 SQ ID
442	6	2.8	175	15	AAU48558	Sequence of mature	515	6	2.8	206	22	AAU50276	Human fibroblast g
443	6	2.8	175	15	AAU58556	Heparin-binding se	516	6	2.8	206	22	AAU50707	Sequence deduced f
444	6	2.8	175	22	AAU1918	C. glutamicum meta	517	6	2.8	207	11	AAU08407	HIV-1 non-subtype
445	6	2.8	175	22	AAU79750	Corynebacterium gl	518	6	2.8	207	21	AAU69359	HIV-1 non-subtype
446	6	2.8	175	22	AAU79994	Corynebacterium gl	519	6	2.8	207	21	AAU87853	Human FGF-6 protei
447	6	2.8	175	22	AAU80015	Corynebacterium gl	520	6	2.8	208	13	AAU24357	HST2 protein encod
448	6	2.8	176	22	AAU00637	Human fibroblast g	521	6	2.8	208	15	AAU58555	Heparin-binding se
449	6	2.8	176	22	AAU00638	Human fibroblast g	522	6	2.8	208	21	AAU69356	HIV-1 non-subtype

523	6	2.8	208	22	ABB69265	Drosophila melanog	596	6	2.8	248	20	AAV31791	Human fibroblast g
524	6	2.8	208	22	ABG65652	Human fibroblast g	597	6	2.8	248	21	AAB53418	Human colon cancer
525	6	2.8	208	22	AAB85817	Human fibroblast g	598	6	2.8	252	22	AAB61133	Human NOV5 protein
526	6	2.8	208	22	AAB85835	Murine fibroblast	599	6	2.8	252	22	AAB61134	Human NOV21 protei
527	6	2.8	208	22	AAB50278	Human FGF-6 SEQ ID	600	6	2.8	252	22	AAB61135	Human NOV22 protei
528	6	2.8	208	22	AAB50708	Human fibroblast g	601	6	2.8	255	21	AAB42698	Human ORFX ORF2462
529	6	2.8	208	22	AAB50708	Human fibroblast g	602	6	2.8	257	20	AAV35468	Chlamydia pneumoni
530	6	2.8	209	21	AAB43342	Human ORFX ORF3106	603	6	2.8	257	22	ABG29649	Novel human diagno
531	6	2.8	209	21	AAG12935	Arabidopsis thalia	604	6	2.8	257	22	AAE03368	Human gene 16 enco
532	6	2.8	209	22	AAG53253	Arabidopsis thalia	605	6	2.8	259	22	ABG63173	Drosophila melanog
533	6	2.8	209	22	ABB11088	Human sialic acid	606	6	2.8	260	21	AAV70244	Human RNA-associat
534	6	2.8	210	12	AAR12262	HIV-1 strain ori o	607	6	2.8	260	22	ABB50208	Human transcriptio
535	6	2.8	210	19	AAW53119	Protein 6 containe	608	6	2.8	260	22	AAB40643	Human polypeptide
536	6	2.8	210	21	AAV77299	HIV-1 (ATCC CRL 85	609	6	2.8	261	22	ABB84703	Drosophila melanog
537	6	2.8	210	22	AAW41065	Human polypeptide	610	6	2.8	261	22	ABG01116	Novel human diagno
538	6	2.8	210	22	AAW41066	Human polypeptide	611	6	2.8	263	22	ABG03873	Novel human diagno
539	6	2.8	210	22	AAW41067	Human polypeptide	612	6	2.8	264	22	AAB85834	Murine fibroblast
540	6	2.8	210	22	AAW68481	HIV-1 strain YBF30	613	6	2.8	265	22	ABG26881	Novel human diagno
541	6	2.8	212	20	AAW01198	Polypeptide fragme	614	6	2.8	265	22	AAE03307	Human gene 16 enco
542	6	2.8	214	22	AAU41669	Propionibacterium	615	6	2.8	265	22	AAE03340	Human lectomedin-2
543	6	2.8	215	20	AAU02349	A representative H	616	6	2.8	266	20	AAV41098	Protein encoded by
544	6	2.8	215	22	AAG63231	Amino acid sequenc	617	6	2.8	266	21	AAB15736	Human FGF-5 protei
545	6	2.8	216	7	AAP60423	Sequence of LAV vi	618	6	2.8	266	21	AAV87852	Human FGF-5 protei
546	6	2.8	216	22	AAE04960	HIV-1 jrf1 Nef pro	619	6	2.8	266	21	AAV87858	Rat fibroblast gro
547	6	2.8	217	22	AAE04962	HIV-1 jrf1 Nef (G2	620	6	2.8	266	21	AAV97887	Drosophila melanog
548	6	2.8	217	22	AAU01268	Brassica napus fat	621	6	2.8	266	22	ABB57832	Encoded by ORF 2 o
549	6	2.8	220	22	AAW41456	Human polypeptide	622	6	2.8	267	9	AAP82964	FGF-3 cDNA clone 1
550	6	2.8	220	22	AAW41457	Human polypeptide	623	6	2.8	267	14	AAW48064	Human fibroblast g
551	6	2.8	224	21	AAV44601	Maize MfO1 protein	624	6	2.8	267	18	AAW22600	Human fibroblast g
552	6	2.8	224	21	AAV86197	Nuclear transport	625	6	2.8	267	22	AAG65651	Human fibroblast g
553	6	2.8	225	21	AAG12934	Arabidopsis thalia	626	6	2.8	267	22	AAE00645	Human fibroblast g
554	6	2.8	225	21	AAG53252	Arabidopsis thalia	627	6	2.8	267	22	AAE00277	Human FGF-5 SEQ ID
555	6	2.8	226	22	AAU33952	Staphylococcus aur	628	6	2.8	267	22	AAE00709	Human fibroblast g
556	6	2.8	226	22	AAW79581	Human protein SEQ	629	6	2.8	268	16	AAE00780	Fibroblast growth
557	6	2.8	229	21	AAB58846	Breast and ovarian	630	6	2.8	268	16	AAE00780	FGF-5. Homo sapie
558	6	2.8	230	20	AAV36134	Human secreted pro	631	6	2.8	268	16	AAE00780	Human FGF-5. Homo
559	6	2.8	230	20	AAV36181	Human secreted pro	632	6	2.8	268	19	AAW5715	Fibroblast growth
560	6	2.8	230	21	AAW06849	Arabidopsis thalia	633	6	2.8	268	19	AAW53031	Fibroblast growth
561	6	2.8	230	21	AAV99378	Human PRO1356 (UNQ	634	6	2.8	268	20	AAV31792	Human fibroblast g
562	6	2.8	230	21	AAV84609	A human membrane	635	6	2.8	268	20	AAV08585	Human FGF-5 protei
563	6	2.8	230	21	AAV51676	Murine clodin 2 pr	636	6	2.8	268	21	AAE10296	Fibroblast growth
564	6	2.8	230	22	AAW09178	Human PRO1356 poly	637	6	2.8	268	21	AAV90414	FGF-5, SEQ ID NO:1
565	6	2.8	230	22	AAU17194	Novel signal trans	638	6	2.8	268	21	AAV32337	Human fibroblast g
566	6	2.8	230	22	AAW38857	Human polypeptide	639	6	2.8	268	22	AAE00636	Human fibroblast g
567	6	2.8	230	22	AAU12417	Human PRO1356 poly	640	6	2.8	268	22	AAE004405	Human fibroblast g
568	6	2.8	230	22	AAE04207	Human gene 10 enco	641	6	2.8	268	22	AAE00642	Human MUSPGF5A pro
569	6	2.8	230	22	AAE04207	Human PRO1356. Ho	642	6	2.8	268	22	AAE00642	Human fibroblast g
570	6	2.8	230	22	AAE04207	Human membrane or	643	6	2.8	268	22	AAE00642	Human fibroblast g
571	6	2.8	230	22	AAE04207	Protein of the inv	644	6	2.8	268	22	AAE00642	FGF5 protein. Hom
572	6	2.8	231	21	AAB43861	Human cancer assoc	645	6	2.8	268	22	AAE00642	Human fibroblast g
573	6	2.8	231	21	AAB43861	Human novel secret	646	6	2.8	268	22	AAE00642	Human fibroblast g
574	6	2.8	231	22	AAU16339	Human colon cancer	647	6	2.8	268	22	AAE00642	Human fibroblast g
575	6	2.8	231	22	AAU16339	Breast and ovarian	648	6	2.8	268	22	AAE00642	Human fibroblast g
576	6	2.8	235	21	AAE05209	Human contig polyp	649	6	2.8	268	22	AAE00642	Human fibroblast g
577	6	2.8	236	11	AAE05209	yeast Ubiquitin hy	650	6	2.8	268	22	AAE00642	Human fibroblast g
578	6	2.8	236	22	AAU30086	Novel human secret	651	6	2.8	268	22	AAE00642	Human fibroblast g
579	6	2.8	236	22	AAU30086	Novel human secret	652	6	2.8	268	22	AAE00642	Human fibroblast g
580	6	2.8	237	16	AAW74336	Helicobacter felis	653	6	2.8	268	22	AAE00642	Human fibroblast g
581	6	2.8	237	17	AAW06729	H. felis structura	654	6	2.8	268	22	AAE00642	Human fibroblast g
582	6	2.8	237	22	ABG23786	Novel human diagno	655	6	2.8	268	22	AAE00642	Human fibroblast g
583	6	2.8	237	22	AAE04961	Human tPA leader p	656	6	2.8	268	22	AAE00642	Human fibroblast g
584	6	2.8	237	22	AAE04961	Human tPA leader p	657	6	2.8	268	22	AAE00642	Human fibroblast g
585	6	2.8	238	18	AAW32796	Esterase protein E	658	6	2.8	268	22	AAE00642	Human fibroblast g
586	6	2.8	238	22	AAE04961	Degr protease. St	659	6	2.8	268	22	AAE00642	Human fibroblast g
587	6	2.8	245	21	AAV92819	C. pneumoniae CPN1	660	6	2.8	268	22	AAE00642	Human fibroblast g
588	6	2.8	245	22	ABG65290	Drosophila melanog	661	6	2.8	268	22	AAE00642	Human fibroblast g
589	6	2.8	245	22	AAU56269	Propionibacterium	662	6	2.8	268	22	AAE00642	Human fibroblast g
590	6	2.8	245	22	ABG03592	Novel human diagno	663	6	2.8	268	22	AAE00642	Human fibroblast g
591	6	2.8	245	22	AAE03592	Human protein tyro	664	6	2.8	268	22	AAE00642	Human fibroblast g
592	6	2.8	246	22	AAE00639	Human fibroblast g	665	6	2.8	268	22	AAE00642	Human fibroblast g
593	6	2.8	246	22	AAE00640	Human fibroblast g	666	6	2.8	268	22	AAE00642	Human fibroblast g
594	6	2.8	247	20	AAV31793	Human fibroblast g	667	6	2.8	268	22	AAE00642	Human fibroblast g
595	6	2.8	247	22	AAU58853	Propionibacterium	668	6	2.8	268	22	AAE00642	Human fibroblast g

669	6	2.8	280	22	ABG10923	Novel human diagno	742	6	2.8	345	21	AAB56897	Human prostate can
670	6	2.8	280	22	AAB99912	Synthetic HIV-deri	743	6	2.8	345	22	AAW83220	C. elegans FATPa si
671	6	2.8	280	22	AAG81165	Mycobacterium tube	744	6	2.8	347	19	AAW37743	S. pneumoniae DDL
672	6	2.8	281	17	AAW08083	Mouse ST-S1, used	745	6	2.8	347	22	AAW75610	Human colon cancer
673	6	2.8	282	17	AAW08084	Human ST-S1, used	746	6	2.8	348	22	AAW75207	Drosophila gustato
674	6	2.8	282	22	AAW61610	Human protein HP03	747	6	2.8	349	21	AAW85691	Murine Sam68-like
675	6	2.8	283	22	ABG01564	Novel human diagno	748	6	2.8	349	22	AAU00912	Staphylococcus hae
676	6	2.8	283	22	ABG01564	Novel human diagno	749	6	2.8	349	22	AAU09332	Murine SLM-1 prote
677	6	2.8	294	22	ABG04225	Novel human diagno	750	6	2.8	350	19	AAW56265	Mouse recombinase
678	6	2.8	294	22	ABG78287	Human BCA-D9, Hom	751	6	2.8	350	21	AAW91933	Murine Rec2 serine
679	6	2.8	295	21	AAW27645	Arabidopsis thalia	752	6	2.8	353	8	AAW70407	ORF 4 gene product
680	6	2.8	295	22	AAW27645	Arabidopsis thalia	753	6	2.8	353	18	AAW34338	Bean golden mosaic
681	6	2.8	296	21	AAW14396	Arabidopsis thalia	754	6	2.8	353	18	AAW34332	Bean golden mosaic
682	6	2.8	296	21	AAW14396	Arabidopsis thalia	755	6	2.8	353	18	AAW34333	Bean golden mosaic
683	6	2.8	298	21	AAW14396	Arabidopsis thalia	756	6	2.8	353	18	AAW34334	Bean golden mosaic
684	6	2.8	302	20	AAU03504	Propionibacterium	757	6	2.8	354	22	ABG23844	Novel human diagno
685	6	2.8	302	20	AAU03504	Propionibacterium	758	6	2.8	354	22	ABG23844	Novel human diagno
686	6	2.8	302	20	AAU03504	Propionibacterium	759	6	2.8	354	22	ABG23844	Novel human diagno
687	6	2.8	302	22	ABG10730	Novel human diagno	760	6	2.8	357	18	AAW34337	Amino acid sequenc
688	6	2.8	302	22	ABG10730	Novel human diagno	761	6	2.8	357	18	AAW34337	Tomato yellow leaf
689	6	2.8	302	22	ABG10730	Novel human diagno	762	6	2.8	357	18	AAW34337	Tomato yellow leaf
690	6	2.8	302	22	ABG10730	Novel human diagno	763	6	2.8	357	18	AAW34337	Tomato yellow leaf
691	6	2.8	303	21	AAW92937	Amino acid sequenc	764	6	2.8	357	18	AAW34331	Human cytokine sequ
692	6	2.8	303	21	AAW92937	Burkholderia strai	765	6	2.8	357	18	AAW34331	Human cytokine sequ
693	6	2.8	304	21	AAW14395	Arabidopsis thalia	766	6	2.8	358	19	AAW44246	Human Wnt-2 proteag
694	6	2.8	304	21	AAW14395	Arabidopsis thalia	767	6	2.8	358	19	AAW44246	Human Wnt-2 proteag
695	6	2.8	306	21	AAW14395	Arabidopsis thalia	768	6	2.8	358	21	AAW44246	Human Wnt-2 proteag
696	6	2.8	306	21	AAW14395	Arabidopsis thalia	769	6	2.8	358	21	AAW44246	Human Wnt-2 proteag
697	6	2.8	308	21	AAW14395	Arabidopsis thalia	770	6	2.8	359	17	AAW44246	Human Wnt-2 proteag
698	6	2.8	309	20	AAW14395	Arabidopsis thalia	771	6	2.8	359	17	AAW44246	Human Wnt-2 proteag
699	6	2.8	309	22	ABG29367	Novel human diagno	772	6	2.8	360	21	AAW44246	Human Wnt-2 proteag
700	6	2.8	310	22	AAW29367	C glutamicum prote	773	6	2.8	360	21	AAW44246	Human Wnt-2 proteag
701	6	2.8	310	22	AAW29367	C glutamicum prote	774	6	2.8	360	21	AAW44246	Human Wnt-2 proteag
702	6	2.8	311	21	AAW29367	S. epidermidis ope	775	6	2.8	360	22	ABG69160	Drosophila melanog
703	6	2.8	312	21	AAW29367	S. epidermidis ope	776	6	2.8	361	18	AAW70562	Product of ORF 4 f
704	6	2.8	312	22	ABG67561	Arabidopsis thalia	777	6	2.8	361	18	AAW70562	Product of ORF 4 f
705	6	2.8	313	22	ABG67561	E. coli cellular p	778	6	2.8	361	18	AAW70562	Product of ORF 4 f
706	6	2.8	313	22	ABG67561	Drosophila melanog	779	6	2.8	361	18	AAW70562	Product of ORF 4 f
707	6	2.8	313	22	ABG67561	Haemophilus influe	780	6	2.8	361	18	AAW70562	Product of ORF 4 f
708	6	2.8	313	22	ABG67561	Streptomyces plica	781	6	2.8	362	22	AAU23384	Novel mottle viru
709	6	2.8	314	21	AAW38739	Arabidopsis thalia	782	6	2.8	362	22	AAU23384	Novel mottle viru
710	6	2.8	314	21	AAW38739	Propionibacterium	783	6	2.8	362	22	AAU23384	Novel mottle viru
711	6	2.8	316	22	AAW58773	Human olfactory re	784	6	2.8	362	22	AAU23384	Novel mottle viru
712	6	2.8	316	22	AAW58773	Human OR-like poly	785	6	2.8	362	22	AAU23384	Novel mottle viru
713	6	2.8	317	18	AAW21949	E6-binding protein	786	6	2.8	362	22	AAU23384	Novel mottle viru
714	6	2.8	317	19	AAW53836	Pseudomonas XpcX s	787	6	2.8	362	22	AAU23384	Novel mottle viru
715	6	2.8	317	21	AAW53836	Pseudomonas XpcX s	788	6	2.8	362	22	AAU23384	Novel mottle viru
716	6	2.8	317	21	AAW53836	Human olfactory re	789	6	2.8	362	22	AAU23384	Novel mottle viru
717	6	2.8	317	21	AAW53836	Human olfactory re	790	6	2.8	362	22	AAU23384	Novel mottle viru
718	6	2.8	318	22	AAW53836	Human OR-like poly	791	6	2.8	362	22	AAU23384	Novel mottle viru
719	6	2.8	318	22	AAW53836	Pseudomonas alcali	792	6	2.8	362	22	AAU23384	Novel mottle viru
720	6	2.8	319	17	AAW53836	Hepatitis C virus	793	6	2.8	362	22	AAU23384	Novel mottle viru
721	6	2.8	321	21	AAW53836	Arabidopsis thalia	794	6	2.8	362	22	AAU23384	Novel mottle viru
722	6	2.8	322	22	AAW53836	Propionibacterium	795	6	2.8	362	22	AAU23384	Novel mottle viru
723	6	2.8	323	22	AAW53836	Human ORF3055	796	6	2.8	362	22	AAU23384	Novel mottle viru
724	6	2.8	323	22	AAW53836	Salmonella typhi c	797	6	2.8	362	22	AAU23384	Novel mottle viru
725	6	2.8	323	22	AAW53836	Human olfactory re	798	6	2.8	362	22	AAU23384	Novel mottle viru
726	6	2.8	323	22	AAW53836	Human olfactory re	799	6	2.8	362	22	AAU23384	Novel mottle viru
727	6	2.8	323	22	AAW53836	Human OR-like poly	800	6	2.8	362	22	AAU23384	Novel mottle viru
728	6	2.8	323	22	AAW53836	Megalomicin biosyn	801	6	2.8	362	22	AAU23384	Novel mottle viru
729	6	2.8	324	20	AAW20352	A representative L	802	6	2.8	362	22	AAU23384	Novel mottle viru
730	6	2.8	324	20	AAW20352	Drosophila melanog	803	6	2.8	362	22	AAU23384	Novel mottle viru
731	6	2.8	324	22	AAW20352	Amino acid sequenc	804	6	2.8	362	22	AAU23384	Novel mottle viru
732	6	2.8	324	22	AAW20352	S. epidermidis ope	805	6	2.8	362	22	AAU23384	Novel mottle viru
733	6	2.8	326	20	AAW20352	A representative L	806	6	2.8	362	22	AAU23384	Novel mottle viru
734	6	2.8	326	21	AAW20352	Amino acid sequenc	807	6	2.8	362	22	AAU23384	Novel mottle viru
735	6	2.8	326	22	AAW20352	Amino acid sequenc	808	6	2.8	362	22	AAU23384	Novel mottle viru
736	6	2.8	326	22	AAW20352	Human secreted pro	809	6	2.8	362	22	AAU23384	Novel mottle viru
737	6	2.8	326	22	AAW20352	Human ORF ORP2376	810	6	2.8	362	22	AAU23384	Novel mottle viru
738	6	2.8	335	22	ABG18780	Novel human diagno	811	6	2.8	362	22	AAU23384	Novel mottle viru
739	6	2.8	337	22	ABG15543	Novel human diagno	812	6	2.8	362	22	AAU23384	Novel mottle viru
740	6	2.8	341	22	ABG38240	Salmonella typhi c	813	6	2.8	362	22	AAU23384	Novel mottle viru
741	6	2.8	341	22	ABG05957	Novel human diagno	814	6	2.8	362	22	AAU23384	Novel mottle viru
			342	22	AAB96671	Putative P. abyss							

815	6	2.8	392	22	ABG06587	Novel human diagno	888	20	AA34696	Chlamydia pneumoni
816	6	2.8	394	19	AAW69713	Streptomyces clavu	889	22	ABG01323	Novel human diagno
817	6	2.8	397	21	AAB43211	Human ORFX ORF2975	890	22	ABY81599	Streptococcus pneu
818	6	2.8	397	22	AGG90285	C glutamicum prote	891	6	AAE10616	Human novel trypsi
819	6	2.8	398	21	AA996307	Human IGFAM-19 imm	892	6	AAE74446	Human protease-inh
820	6	2.8	398	22	ABBS58306	Drosophila melanog	893	6	AAE10618	Human novel trypsi
821	6	2.8	400	22	AAW75203	Tyrosine phosphata	894	6	AAE10619	Human novel trypsi
822	6	2.8	400	16	AAW42064	Human polypeptide	895	6	AAE10619	Human novel trypsi
823	6	2.8	401	12	AAE12130	ORF 2 of Igg light	896	6	AAE15174	Streptococcus pneu
824	6	2.8	401	22	AAU71917	C. glutamicum meta	897	6	AAE81224	Mycobacterium tube
825	6	2.8	401	22	ABG15468	Novel human diagno	898	6	AAE44242	Human cell signall
826	6	2.8	401	22	AGG92077	C glutamicum prote	899	6	ABE68500	Drosophila melanog
827	6	2.8	401	22	AAW79749	Corynebacterium gl	900	6	AAU49979	Propionibacterium
828	6	2.8	401	22	AAW79993	Corynebacterium gl	901	6	AAE31891	Helicobacter pylor
829	6	2.8	401	22	AAB80014	Corynebacterium gl	902	6	AAW20085	Helicobacter pylor
830	6	2.8	407	22	ABG29590	Novel human diagno	903	6	AAE00224	Sus scrofa PrKag3
831	6	2.8	409	21	AAAG49705	Aradidopsis thalia	904	6	AAE51422	Novel human diagno
832	6	2.8	411	20	AAAG02353	A representative L	905	6	AAE02096	Novel human diagno
833	6	2.8	411	22	AAAG3225	Amino acid sequenc	906	6	AAU27781	Human full-length
834	6	2.8	413	20	AAAG02335	A representative L	907	6	AAU27781	Human full-length
835	6	2.8	413	22	AAAG63237	Amino acid sequenc	908	6	AAE23661	Novel human enzyme
836	6	2.8	415	19	AAW69228	Human lysosomal si	909	6	AAE53796	Novel human enzyme
837	6	2.8	415	21	AAB43114	Human ORFX ORF2878	910	6	AAW72229	Aradidopsis thalia
838	6	2.8	415	21	AAAG29794	Aradidopsis thalia	911	6	AAE52122	Aradidopsis thalia
839	6	2.8	415	21	AAE85276	C. albicans CalR10	912	6	AAE25881	Human secreted pro
840	6	2.8	415	22	ABE68007	Drosophila melanog	913	6	AAE48359	Mycobacterium tube
841	6	2.8	415	22	AAW76774	Corynebacterium gl	914	6	AAE30629	Aradidopsis thalia
842	6	2.8	418	22	AAU35812	Helicobacter pylor	915	6	ABG01344	Novel human diagno
843	6	2.8	418	22	ABG03314	Novel human diagno	916	6	AAE37729	Chlamydia trachoma
844	6	2.8	419	18	AAW26465	Mycobacterial sery	917	6	ABE59524	Drosophila trachoma
845	6	2.8	419	22	AAE81240	Mycobacterium tube	918	6	AAE37783	Streptococcus pneu
846	6	2.8	421	22	ABG20221	Novel human diagno	919	6	AAE73937	Human prostate tum
847	6	2.8	424	22	ABE60996	Drosophila melanog	920	6	AAE21384	Aradidopsis thalia
848	6	2.8	425	22	ABE68588	Drosophila melanog	921	6	AAE21384	Aradidopsis thalia
849	6	2.8	426	18	AAW20811	H. pylori inner me	922	6	AAE94571	Human protein sequ
850	6	2.8	426	21	AAE53602	Aradidopsis thalia	923	6	AAE30628	Aradidopsis thalia
851	6	2.8	436	17	AAW03662	Human 70K UI snRNP	924	6	AAE30628	Aradidopsis thalia
852	6	2.8	436	20	AAU22342	70K UI snRNA bindi	925	6	AAE30628	Aradidopsis thalia
853	6	2.8	440	21	AAE31611	Aradidopsis thalia	926	6	AAE91728	C glutamicum prote
854	6	2.8	442	21	AAE56372	Human prostate can	927	6	AAE91728	C glutamicum prote
855	6	2.8	442	21	AAE53601	Aradidopsis thalia	928	6	AAE03082	Novel human diagno
856	6	2.8	443	22	AAU30139	Novel human secret	929	6	AAU28257	Human plant homeod
857	6	2.8	443	22	ABE61688	Drosophila melanog	930	6	ABG14031	Novel human secret
858	6	2.8	446	21	AAE53797	Aradidopsis thalia	931	6	AAE04955	Mycobacterium spec
859	6	2.8	447	22	AAE72391	Barley LHRT1 encode	932	6	AAE27327	A. thaliana NIM1 h
860	6	2.8	449	22	AAE68879	Human RECAP polype	933	6	AAE25670	hNET sequence enco
861	6	2.8	450	19	AAW46606	Tyrosine kinase as	934	6	AAW46758	Amino acid sequenc
862	6	2.8	450	20	AAE29635	Human tyrosine kin	935	6	AAE01924	Aradidopsis thalia
863	6	2.8	450	20	AAE221930	Human tyrosine kin	936	6	AAE76840	Aradidopsis thalia
864	6	2.8	450	22	ABG21667	Novel human diagno	937	6	ABG21351	Aradidopsis thalia
865	6	2.8	452	22	AAE70913	S cerevisiae apopt	938	6	AAE49311	Aradidopsis thalia
866	6	2.8	453	21	AAE94340	Human cell surface	939	6	AAE01924	Aradidopsis thalia
867	6	2.8	453	22	AAE91881	C glutamicum prote	940	6	AAE55964	Full length human
868	6	2.8	457	22	ABG11888	Novel human diagno	941	6	AAE59128	Human serine/threo
869	6	2.8	458	22	AAU18482	Human endocrine po	942	6	AAE59128	H. pylori transpor
870	6	2.8	459	22	ABG29005	Novel human diagno	943	6	AAE20918	Drosophila melanog
871	6	2.8	459	22	ABG29867	Novel human diagno	944	6	ABE60224	Escherichia coli F
872	6	2.8	462	12	AAE12401	Enantioselective a	945	6	AAE52370	Escherichia coli F
873	6	2.8	462	13	AAE25320	Enantioselective a	946	6	AAE21383	Aradidopsis thalia
874	6	2.8	464	22	AAE00222	Pig AMPK gamma sub	947	6	AAE31083	Aradidopsis thalia
875	6	2.8	466	19	AAW72230	Drosophila gamma sub	948	6	AAE39498	Aradidopsis thalia
876	6	2.8	466	22	ABE70578	HSV-2 strain SB5 C	949	6	AAE27306	Human polypeptide
877	6	2.8	468	20	AAE29114	Drosophila melanog	950	6	AAE91159	A. thaliana NIM1 h
878	6	2.8	468	22	ABE58174	Amino acid sequenc	951	6	AAE81783	C glutamicum prote
879	6	2.8	470	22	ABE58174	Novel human diagno	952	6	AAE56098	Human protein tyro
880	6	2.8	471	22	AAE49242	Propionibacterium	953	6	AAU42195	LAR tyrosine phosph
881	6	2.8	477	19	AAW80695	S. pneumoniae hydr	954	6	AAU41279	Propionibacterium
882	6	2.8	479	22	ABE62334	Drosophila melanog	955	6	AAE72228	Fusion protein con
883	6	2.8	482	22	ABG24912	Novel human diagno	956	6	AAE53795	HSV-2 strain SB5 C
884	6	2.8	484	22	AAU68515	Human novel cytoki	957	6	ABG28986	Aradidopsis thalia
885	6	2.8	484	22	AAE92676	C glutamicum prote	958	6	AAE28984	Novel human diagno
886	6	2.8	484	22	AAE79356	Corynebacterium gl	959	6	AAE42369	Novel human diagno
887	6	2.8	485	21	AAE44741	Aradidopsis thalia	960	6	AAE82630	Human ORFX ORF2133
										70K autoantigen, p
										Amino acid sequenc

961	6	2.8	615	22	AAM79654	Human protein SEQ
962	6	2.8	616	22	AAM41284	Human polypeptide
963	6	2.8	616	20	AAV35424	Amino acid sequenc
964	6	2.8	618	13	AAR29928	Eimeria antigen Ea
965	6	2.8	618	19	AAW58566	Eimeria acervulina
966	6	2.8	620	22	ABG19308	Novel human diagno
967	6	2.8	622	22	AAM78670	Human protein SEQ
968	6	2.8	625	21	AAV92331	Human Trk oncogene
969	6	2.8	626	21	AAV88485	DraIII methylase D
970	6	2.8	627	22	AAU51580	Propionibacterium
971	6	2.8	628	21	AAG44740	Arabidopsis thalia
972	6	2.8	629	21	AAG48916	Arabidopsis thalia
973	6	2.8	631	22	AAU15923	Human novel secret
974	6	2.8	632	21	AAB26946	Wheat auxin transp
975	6	2.8	632	22	AAM40047	Human polypeptide
976	6	2.8	635	16	AAR74633	Nr (never ripe) to
977	6	2.8	635	16	AAR74629	Tomato ethylene re
978	6	2.8	635	19	AAW73125	Tomato ethylene re
979	6	2.8	635	19	AAW73124	Tomato ethylene re
980	6	2.8	636	20	AAW99183	Rhodococcus corall
981	6	2.8	637	18	AAW36182	Monkey p53 tumour
982	6	2.8	637	21	AAV97052	Rhodococcus sp. oh
983	6	2.8	639	21	AAG48915	Arabidopsis thalia
984	6	2.8	645	21	AAG21382	Arabidopsis thalia
985	6	2.8	645	21	AAG48914	Arabidopsis thalia
986	6	2.8	646	21	AAV31082	Arabidopsis thalia
987	6	2.8	646	22	ABW64598	Drosophila melanog
988	6	2.8	647	22	AAM23746	Human EST encoded
989	6	2.8	647	22	AAU14379	Human novel protei
990	6	2.8	649	19	AAW72097	HSV-2 strain S85 C
991	6	2.8	650	20	AAV14962	Amino acid sequenc
992	6	2.8	650	22	AAW83262	C elegans FATPa SE
993	6	2.8	650	22	AAW83274	C elegans FATPa SE
994	6	2.8	652	15	AAW63808	Human amphotropic
995	6	2.8	652	19	AAW70499	Human sodium-lithi
996	6	2.8	655	22	AAW83263	C elegans FATPB SE
997	6	2.8	660	16	AAW69633	Human interleukin-
998	6	2.8	660	21	AAW54249	Human pancreatic c
999	6	2.8	662	16	AAW69632	Human interleukin-
1000	6	2.8	662	18	AAW12772	Human interleukin-

ALIGNMENTS

RESULT 1
AAB18635
ID AAB18635 standard; Protein; 211 AA.
XX AAB18635;
DT 22-JAN-2001 (first entry)
XX Amino acid sequence of human fibroblast growth factor (FGF)-20.
DE
XX pD10-VEGFuc; gene delivery vector; eye disease; neovascular disease;
KW neurotrophic factor; anti-angiogenic factor; eye disease; glaucoma;
KW macular degeneration; diabetic retinopathy; retinitis pigmentosa;
KW inherited retinal degeneration; surgery-induced retinopathy;
KW retinal detachment; photic retinopathy; toxic retinopathy;
KW trauma-induced retinopathy; wet age related macular degeneration;
KW ARMD; retinopathy; fibroblast growth factor-20; FGF-20.
XX
XX Homo sapiens.
XX
XX WO200054813-A2.
PN
XX
XX 21-SEP-2000.
PD
XX
XX 15-MAR-2000; 2000WO-US07062.
PF
XX
XX 15-MAR-1999; 99US-0124460.
PR
XX 06-JAN-2000; 2000US-0174984.

XX	(CHIR) CHIRON CORP.	
PA	(REGC) UNIV CALIFORNIA.	
XX	Manning WC, Dwarki VJ, Rendahl K, Zhou S, McGee LH, Lau D;	
PI	Flannery JG, Miller S, Wang F, Di Polo A;	
XX	WPI; 2000-618862/59.	
DR	N-PSDB; AAA75630.	
XX	Treating or preventing eye diseases or inhibiting neovascular disease	
PT	of the eye, comprises intraocularly administering a gene delivery	
PT	vector that directs expression of neurotrophic factors or	
PT	anti-angiogenic factors -	
XX	Disclosure; Fig 29; 86pp; English.	
PS		
XX	The present sequence represents human fibroblast growth factor (FGF)-20.	
CC	FGF-20 is expressed using a gene delivery vector of the invention.	
CC	Vectors of the invention are used for treating or preventing eye	
CC	diseases, or inhibiting neovascular disease of the eye. The gene	
CC	delivery vector directs the expression of one or more neurotrophic	
CC	factors, or anti-angiogenic factors, such that the disease of the eye	
CC	is prevented or treated. The gene delivery vectors are useful for	
CC	treating or preventing diseases of the eye such as macular degeneration,	
CC	diabetic retinopathy, inherited retinal degeneration such as retinitis	
CC	pigmentosa, glaucoma, surgery-induced retinopathy, retinal detachment,	
CC	photic retinopathy, toxic retinopathy or trauma-induced retinopathy and	
CC	for inhibiting neovascular diseases such as wet age related macular	
CC	degeneration (ARMD) or retinopathy of prematurity.	
XX	SQ Sequence 211 AA;	
XX	Query Match 100.0%; Score 211; DB 21; Length 211;	
XX	Best Local Similarity 100.0%; Pred. No. 1.1e-202;	
XX	Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 MAPLAEVGGFTGLGELGQQVGSFLLPPAGERPPLGERSAAERSARGGPGAQIAHL 60	
Db	1 MAPLAEVGGFTGLGELGQQVGSFLLPPAGERPPLGERSAAERSARGGPGAQIAHL 60	
Qy	61 HGILRRRLYCRTHFLQILPDGSGVQGTRODHSFLGILEFTSVAVLVSIRGVDSGLYLG 120	
Db	61 HGILRRRLYCRTHFLQILPDGSGVQGTRODHSFLGILEFTSVAVLVSIRGVDSGLYLG 120	
Qy	121 MNDKGLYSGEKLTSCEIFRQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDCA 180	
Db	121 MNDKGLYSGEKLTSCEIFRQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDCA 180	
Qy	181 SKRHOKFTHFILPRVPDPERVPELYKDLLMYT 211	
Db	181 SKRHOKFTHFILPRVPDPERVPELYKDLLMYT 211	
XX	RESULT 2	
AAU09931	AAU09931 standard; Protein; 211 AA.	
XX	AC AAU09931;	
XX	15-JAN-2002 (first entry)	
DT	Human fibroblast growth factor-like (FGF-L) polypeptide sequence.	
XX	Human; fibroblast growth factor-like; FGF-L; agonist; antagonist;	
XX	vulnerable; virucide; hepatotropic; antiinflammatory; gut disorder;	
XX	hepatitis; diabetes; wound healing; ulcer; liver disorder;	
XX	lung disorder; angiogenesis.	
XX	Homo sapiens.	
XX	WO200168854-A2.	
PN		
XX		

PD 20-SEP-2001.
XX
PF 13-MAR-2001; 2001WO-US08013.
XX
PR 13-MAR-2000; 2000US-188786P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Jing S, Bass MB;
XX
XX WPI; 2001-596910/67.
DR N-PSDB; AAS15701.
XX
XX New fibroblast growth factor-like polypeptide and polynucleotide for
PT diagnosis, prevention and treatment of diseases, disorders or
PT conditions involving the central nervous system, teeth, heart, liver or
PT adipose tissue -
XX
XX Claim 3; Fig 1; 116pp; English.
PS
XX
XX The present invention relates to new isolated fibroblast growth
CC factor-like (FGF-L) nucleic acid molecules and polypeptides. The FGF-L
CC polypeptide is useful for determining whether a compound inhibits FGF-L
CC polypeptide, and also for identifying a compound that binds to the
CC polypeptide. The FGF-L polypeptides of the invention are useful for
CC treating, preventing or ameliorating a medical condition or an FGF-L
CC polypeptide-related disease, condition or disorder such as wound healing
CC disorders, ulcers, gut disorders, lung disorders, liver disorders such as
CC hepatitis and diabetes. The invention is also useful for diagnosing a
CC pathological condition or susceptibility to a pathological condition in
CC a subject and is useful for modulating levels of FGF-L in an animal.
CC Other uses are detecting or quantifying the amount of FGF-L polypeptide
CC and for identifying or developing novel agonists and antagonists of the
CC FGF-L polypeptide signalling pathway which are useful for treating one
CC or more diseases or disorders, and also as an immunogen for producing
CC antibodies for in vivo imaging. The present sequence encodes the human
CC FGF-L polypeptide of the invention. The present sequence represents the
CC human FGF-L polypeptide of the invention.
XX
XX
SQ Sequence 211 AA;
Query Match 100.0%; Score 211; DB 22; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.le-202;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPLAEVGGFLGGLGQGVGSHFLPPAGERPPLLGERRSAERSARGGPGAAQLAHL 60
DB 1 MAPLAEVGGFLGGLGQGVGSHFLPPAGERPPLLGERRSAERSARGGPGAAQLAHL 60
QY 61 HGILRRQLYCRGTFHQLQLPDGVSQGTQDHSLSFGILEFISVAVGLVSIKGVDSGLYL 120
DB 61 HGILRRQLYCRGTFHQLQLPDGVSQGTQDHSLSFGILEFISVAVGLVSIKGVDSGLYL 120
QY 121 MNDKGLYSGEKLTSCEIFREQEENWNTYSSNIYKHGDTGRRYFVALNKDGTFRDGR 180
DB 121 MNDKGLYSGEKLTSCEIFREQEENWNTYSSNIYKHGDTGRRYFVALNKDGTFRDGR 180
QY 181 SKRHQKFTFLPRPVDPERVPELYKDLLMYT 211
DB 181 SKRHQKFTFLPRPVDPERVPELYKDLLMYT 211
RESULT 3
AAG65666
ID AAG65666 standard; protein; 211 AA.
XX
XX AAG65666;
XX
XX 07-JAN-2002 (first entry)
XX
XX Human fibroblast growth factor (FGF)-20.
DE Human fibroblast growth factor (FGF)-20.
XX Fibroblast growth factor; FGF; FGF-like polypeptide; mitogenic;
KW

KW fat deposition; vulnery; antiulcer; dermatological; anorectic;
KW antidiabetic; antiinflammatory; cytostatic; hepatic; virucide;
KW neuroprotectant; pulmonary; gene therapy; vaccine; human.
OS
XX Homo sapiens.
XX
PN WO200172957-A2.
XX
XX 04-OCT-2001.
XX
PF 02-APR-2001; 2001WO-IB00664.
XX
PR 31-MAR-2000; 2000US-0540118.
XX
PA (ITOH/) ITOH N.
XX
PI Itoh N;
XX
XX WPI; 2001-611623/70.
XX
XX New human nucleic acid encoding fibroblast growth factor-like peptide,
PT useful for treatment and diagnosis of e.g. wounds and inflammatory
PT bowel disease -
XX
XX Disclosure; Fig 3; 172pp; English.
XX
XX The invention provides human nucleic acids encoding fibroblast growth
CC factor (FGF)-like peptide. The FGF-like polypeptides can be expressed by
CC standard recombinant methodology and are mitogenic for a wide range of
CC cells, inducing differentiation and proliferation, and inhibiting
CC deposition of fat. The FGF-like polypeptides, polynucleotides and
CC specific antibodies and modulators are useful for treating a very wide
CC range of diseases and conditions, e.g. wounds, ulcers, skin aging,
CC obesity, diabetes, alopecia, inflammatory bowel disease, emphysema, viral
CC hepatitis, multiple sclerosis, respiratory distress syndrome, tumors of
CC the eye, etc., also for maintaining organs before transplant and
CC supporting culture of primary cells and tissues. Sequences AAG65647-67
CC represent amino acid sequences of some members of the FGF family.
XX
SQ Sequence 211 AA;
Query Match 100.0%; Score 211; DB 22; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.le-202;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPLAEVGGFLGGLGQGVGSHFLPPAGERPPLLGERRSAERSARGGPGAAQLAHL 60
DB 1 MAPLAEVGGFLGGLGQGVGSHFLPPAGERPPLLGERRSAERSARGGPGAAQLAHL 60
QY 61 HGILRRQLYCRGTFHQLQLPDGVSQGTQDHSLSFGILEFISVAVGLVSIKGVDSGLYL 120
DB 61 HGILRRQLYCRGTFHQLQLPDGVSQGTQDHSLSFGILEFISVAVGLVSIKGVDSGLYL 120
QY 121 MNDKGLYSGEKLTSCEIFREQEENWNTYSSNIYKHGDTGRRYFVALNKDGTFRDGR 180
DB 121 MNDKGLYSGEKLTSCEIFREQEENWNTYSSNIYKHGDTGRRYFVALNKDGTFRDGR 180
QY 181 SKRHQKFTFLPRPVDPERVPELYKDLLMYT 211
DB 181 SKRHQKFTFLPRPVDPERVPELYKDLLMYT 211
RESULT 4
AAU02081
ID AAU02081 standard; Protein; 211 AA.
XX
XX AAU02081;
XX
XX 07-SEP-2001 (first entry)
XX
XX Human fibroblast growth factor 20, FGF-20.
DE Human fibroblast growth factor 20; FGF-20; Parkinson's disease;
XX
KW

KW		substantia nigra; dopaminergic neuron; cochlea-associated disease;
KW		otosclerosis; Cogan's syndrome; Meniere's disease; Pendred's syndrome;
KW		diabetes-associated hearing loss; congenital malformations;
KW		autoimmune disease-related hearing loss; age-related hearing loss;
KW		deafness; ischaemia-related hearing disturbance; immunogen;
KW		antibody; neuro-degenerative disease; tendonitis; wound healing;
KW		stroke; ischaemia.
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Binding-site	170..186
FT	/label=	Heparin_binding_site
XX		
PX	WO200131008-A2.	
PN		
PD	03-MAY-2001.	
XX		
PF	20-OCT-2000; 2000MO-US29237.	
XX		
PR	22-OCT-1999; 99US-0161162.	
PR	08-MAR-2000; 2000US-0187856.	
PA	(CHIR) CHIRON CORP.	
PA	(KYOU) UNIV KYOTO.	
XX		
PI	Itoh N, Kavanaugh WM;	
FI	MP1; 2001-308642/32.	
DR	N-P5DB; AAS03277.	
DR		
XX	New human and rat Fibroblast Growth Factor (FGF) polypeptides for	
PT	providing trophic support for cells used in Parkinson patients, and	
PT	alleviating brain and cochlea conditions -	
XX		
PS	Claim 12; Fig 8; 73pp; English.	
XX		
CC	The sequence is Human fibroblast growth factor 20, FGF-20. The FGF	
CC	polypeptides and nucleic acids encoding them are useful for providing	
CC	trophic support for cells in a patient, especially a patient with	
CC	Parkinson's disease, and FGF-20 is additionally used to treat patients	
CC	with conditions of the substantia nigra. The polypeptides and nucleic	
CC	acids are useful for alleviating human brain conditions by slowing	
CC	degeneration, restoring function of, or increasing the number of,	
CC	dopaminergic neurons. The polypeptides and nucleic acids are also	
CC	useful for alleviating cochlea-associated disease by slowing	
CC	degeneration of or restoring or maintaining normal function of the	
CC	structure of cochlea, where the disease is otosclerosis, Cogan's	
CC	syndrome, Meniere's disease, Pendred's syndrome, diabetes-associated	
CC	hearing loss, congenital malformations, autoimmune disease-related	
CC	hearing loss, age-related hearing loss, deafness associated with lack	
CC	of FGF receptor and ischemia-related hearing disturbance. Other	
CC	diseases thought to be amenable to FGF therapeutic activity include	
CC	neuro-degenerative diseases, tendonitis, wound healing, stroke and	
CC	ischaemia. The polypeptides can be used to screen for agonists and	
CC	antagonists. Epitope bearing fragments of the FGF-20 polypeptides can be	
CC	used to raise anti-FGF-20 antibodies.	
XX		
SQ	Sequence 211 AA;	
	Query Watch	Score 211; DB 22; Length 211;
	Best Local Similarity	100.0%; Pred. No. 1.le-202;
	Matches 211; Conservative	0; Mismatches 0; Indels 0; Gaps
Qy	1 MAPLAEVGSGFLGGLEGCGVGSHELLPPAGERPPLLCGRSSAAERSARGGPQAQLAHL 60	
Db	1 MAPLAEVGSGFLGGLEGCGVGSHELLPPAGERPPLLCGRSSAAERSARGGPQAQLAHL 60	
Qy	61 HGILRRRLQYCRTHGLIQLPDGVSOGTRQDHSLSGLEIFISVAVGLVSRGVDSGLYLIG 120	
Db	61 HGILRRRLQYCRTHGLIQLPDGVSOGTRQDHSLSGLEIFISVAVGLVSRGVDSGLYLIG 120	
Qy	121 MNDKGELYSSEKLSSECIFRQEENWNTYSNVTYKKHGDTGRFYFVALNKDGTPRDGAR 180	

CC increasing agents, or for treating cerebral nervous diseases. The present
CC sequence represents the human FGF-CX protein.
XX
SQ Sequence 211 AA;

Query Match 100.0%; Score 211; DB 22; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.1e-202;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAPLAEVGFLGLEGQGVSHFLLPAGERPPLGERSAERSARGGPAQAHL 60
Db 1 MAPLAEVGFLGLEGQGVSHFLLPAGERPPLGERSAERSARGGPAQAHL 60
Qy 61 HGILRRQLYCRFTGFLQILPDGVSQGTQDHSFLGILFISVAVGLSVIRGVDGSLYL 120
Db 61 HGILRRQLYCRFTGFLQILPDGVSQGTQDHSFLGILFISVAVGLSVIRGVDGSLYL 120
Qy 121 MNDKGYLGSEKLTSECIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGR 180
Db 121 MNDKGYLGSEKLTSECIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGR 180
Qy 181 SKRHQKFTFLPRPDPVPELYKDLLMYT 211
Db 181 SKRHQKFTFLPRPDPVPELYKDLLMYT 211

RESULT 6

AAU02080
ID AAU02080 standard; Protein: 212 AA.

XX AAU02080;
AC
CC
DT 07-SEP-2001 (first entry)
DE Rat fibroblast growth factor 20, FGF-20.
XX
KW Rat; fibroblast growth factor 20; FGF-20; Parkinson's disease;
KW substantia nigra; dopaminergic neuron; cochlea-associated disease;
KW otosclerosis; Cogan's syndrome; Meniere's disease; Pendred's syndrome;
KW diabetes-associated hearing loss; congenital malformations;
KW autoimmune disease-related hearing loss; age-related hearing loss;
KW deafness; ischaemia-related hearing disturbance; immunogen;
KW antibody; neuro-degenerative disease; tendonitis; wound healing;
KW stroke; ischaemia.

XX Rattus sp.

XX Key Location/Qualifiers
FH Peptide 56..70
FT /label= Epitope
FT /note= "Peptide used to raise anti-FGF-20 antibodies"
FT Binding-site 170..186
FT /label= Heparin_binding_site
FT Peptide 176..189
FT /label= Epitope
FT /note= "Peptide used to raise anti-FGF-20 antibodies"

XX WO200131008-A2.

XX 03-MAY-2001.

XX 20-OCT-2000; 2000WO-US29237.

XX 22-OCT-1999; 99US-0161162.

XX 08-MAR-2000; 2000US-0187856.

XX (CHIR) CHIRON CORP.

XX (KYOU) UNIV KYOTO.

XX Itoh N, Kavanaugh WM;

XX WPI: 2001-308642/32.

XX N-PSDB; AAS03276.

XX New human and rat Fibroblast Growth Factor (FGF) polypeptides for
PT providing trophic support for cells used in Parkinson patients, and
PT alleviating brain and cochlea conditions -
XX
XX Claim 45; Fig 7; 73pp; English.

XX The sequence is Rat fibroblast growth factor 20, FGF-20. The FGF
CC polypeptides and nucleic acids encoding them are useful for providing
CC trophic support for cells in a patient, especially a patient with
CC Parkinson's disease, and FGF-20 is additionally used to treat patients
CC with conditions of the substantia nigra. The polypeptides and nucleic
CC acids are useful for alleviating human brain conditions by slowing
CC degeneration, restoring function of, or increasing the number of,
CC dopaminergic neurons. The polypeptides and nucleic acids are also
CC useful for alleviating cochlea-associated disease by slowing of the
CC degeneration of or restoring or maintaining normal function of the
CC structure of cochlea, where the disease is otosclerosis, Cogan's
CC syndrome, Meniere's disease, Pendred's syndrome, diabetes-associated
CC hearing loss, congenital malformations, autoimmune disease-related
CC hearing loss, age-related hearing loss, deafness associated with lack
CC of FGF receptor and ischaemia-related hearing disturbance. Other
CC diseases thought to be amenable to FGF therapeutic activity include
CC neuro-degenerative diseases, tendonitis, wound healing, stroke and
CC ischaemia. The polypeptides can be used to screen for agonists and
CC antagonists. Epitope bearing fragments of the FGF-20 polypeptides can be
CC used to raise anti-FGF-20 antibodies.

XX Sequence 212 AA;

Query Match 40.3%; Score 85; DB 22; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.1e-76;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 KGELYGSEKLTSECIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGRSKR 183
Db 124 KGELYGSEKLTSECIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGRSKR 183

Qy 184 HQTFTFLPRPDPVPELYKDLL 208

Db 184 HQTFTFLPRPDPVPELYKDLL 208

RESULT 7

AAAR56503
ID AAAR56503 standard; peptide; 142 AA.

XX AAAR56503;

XX 06-MAR-1995 (first entry)

XX Glia activating factor (GAF) peptide.

XX Glia activating factor; GAF; testing; detection; antibody; cancer;
KW osteogenesis; platelet; hepatopathy; cirrhosis; anticancer agent.

XX Homo sapiens.

XX EP608546-A.

XX 03-AUG-1994.

XX 18-DEC-1993; 93EP-0120491.

XX 22-DEC-1992; 92JP-0342100.

XX 23-AUG-1993; 93JP-0207719.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Kurokawa T, Kuroshima K, Seko C, Yoshitomi S;

XX WPI: 1994-242006/30.

PT New glia activating factor polypeptide and antibodies - for use
 PT in detection, purification and treatment of diseases, e.g. as
 PT anticancer or platelet-increasing agents.

XX
 XX Disclosure; Page 38-39; 80pp; English.

CC The glia activating factor (GAF) polypeptides (See AAR56503-56511) can
 CC be used as platelet increasing agents, osteogenesis promoting
 CC agents or for treating cerebral nervous diseases or hepatopathy such
 CC as hepatic cirrhosis. They can also be used to treat cancer when
 CC used alongside an anticancer agent. Antibodies directed against the
 CC GAF polypeptides can be used for detecting or determining a
 CC biological activity of a GAF polypeptide or for purifying a GAF
 CC polypeptide. The antibodies, which also neutralise the cell growth
 CC activity of GAF, can be used as anticancer agents.

XX
 XX Sequence 142 AA;

Query Match 9.0%; Score 19; DB 15; Length 142;
 Best Local Similarity 100.0%; Pred. No. 7.5e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 AVGLVSIRGVDSGLYLGMM 122
 |||||
 Db 48 AVGLVSIRGVDSGLYLGMM 66

RESULT 8
 AAR56510

ID AAR56510 standard; peptide; 159 AA.

XX
 AC AAR56510;

XX
 DT 06-MAR-1995 (first entry)

XX
 DE Glia activating factor (GAF) peptide.

XX
 KW Glia activating factor; GAF; testing; detection; antibody; cancer;
 KW osteogenesis; platelet; hepatopathy; cirrhosis; anticancer agent.

XX
 OS Homo sapiens.

XX
 PN EP608546-A.

XX
 PD 03-AUG-1994.

XX
 PF 18-DEC-1993; 93EP-0120491.

XX
 PR 22-DEC-1992; 92JP-0342100.

XX
 PR 23-AUG-1993; 93JP-0207719.

XX
 PA (TAKE) TAKEDA CHEM IND LTD.

XX
 PI Kurokawa T, Kuroshima K, Seko C, Yoshitomi S;

XX
 DR WPI; 1994-242006/30.

XX
 PT New glia activating factor polypeptide and antibodies - for use
 PT in detection, purification and treatment of diseases, e.g. as
 PT anticancer or platelet-increasing agents.

XX
 PS Disclosure; Page 45; 80pp; English.

XX The glia activating factor (GAF) polypeptides (See AAR56503-56511) can
 CC be used as platelet increasing agents, osteogenesis promoting
 CC agents or for treating cerebral nervous diseases or hepatopathy such
 CC as hepatic cirrhosis. They can also be used to treat cancer when
 CC used alongside an anticancer agent. Antibodies directed against the
 CC GAF polypeptides can be used for detecting or determining a
 CC biological activity of a GAF polypeptide or for purifying a GAF
 CC polypeptide. The antibodies, which also neutralise the cell growth
 CC activity of GAF, can be used as anticancer agents.

XX

SQ Sequence 159 AA;

Query Match 9.0%; Score 19; DB 15; Length 159;
 Best Local Similarity 100.0%; Pred. No. 8.3e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 AVGLVSIRGVDSGLYLGMM 122
 |||||
 Db 52 AVGLVSIRGVDSGLYLGMM 70

RESULT 9

AAR56511

ID AAR56511 standard; peptide; 160 AA.

XX
 AC AAR56511;

XX
 DT 06-MAR-1995 (first entry)

XX
 DE Glia activating factor (GAF) peptide.

XX
 KW Glia activating factor; GAF; testing; detection; antibody; cancer;
 KW osteogenesis; platelet; hepatopathy; cirrhosis; anticancer agent.

XX
 OS Homo sapiens.

XX
 PN EP608546-A.

XX
 PD 03-AUG-1994.

XX
 PF 18-DEC-1993; 93EP-0120491.

XX
 PR 22-DEC-1992; 92JP-0342100.

XX
 PR 23-AUG-1993; 93JP-0207719.

XX
 PA (TAKE) TAKEDA CHEM IND LTD.

XX
 PI Kurokawa T, Kuroshima K, Seko C, Yoshitomi S;

XX
 DR WPI; 1994-242006/30.

XX
 PT New glia activating factor polypeptide and antibodies - for use
 PT in detection, purification and treatment of diseases, e.g. as
 PT anticancer or platelet-increasing agents.

XX
 PS Disclosure; Page 46; 80pp; English.

XX The glia activating factor (GAF) polypeptides (See AAR56503-56511) can
 CC be used as platelet increasing agents, osteogenesis promoting
 CC agents or for treating cerebral nervous diseases or hepatopathy such
 CC as hepatic cirrhosis. They can also be used to treat cancer when
 CC used alongside an anticancer agent. Antibodies directed against the
 CC GAF polypeptides can be used for detecting or determining a
 CC biological activity of a GAF polypeptide or for purifying a GAF
 CC polypeptide. The antibodies, which also neutralise the cell growth
 CC activity of GAF, can be used as anticancer agents.

SQ Sequence 160 AA;

Query Match 9.0%; Score 19; DB 15; Length 160;
 Best Local Similarity 100.0%; Pred. No. 8.3e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 AVGLVSIRGVDSGLYLGMM 122
 |||||
 Db 53 AVGLVSIRGVDSGLYLGMM 71

RESULT 10

AAR56508

ID AAR56508 standard; peptide; 175 AA.

XX
 AC AAR56508;

```

XX 06-MAR-1995 (first entry)
DT
XX
XX Glia activating factor (GAF) peptide.
DE
XX
XX Glia activating factor; GAF; testing; detection; antibody; cancer;
KW osteogenesis; platelet; hepatopathy; cirrhosis; anticancer agent.
KW
XX
XX Homo sapiens.
OS
XX
XX EP608546-A.
PN
XX
XX 03-AUG-1994.
PD
XX
XX 18-DEC-1993; 93EP-0120491.
PF
XX
XX 22-DEC-1992; 92JP-0342100.
PR
XX
XX 23-AUG-1993; 93JP-0207719.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
PA
XX
XX Kurokawa T, Kuroshima K, Seko C, Yoshitomi S;
PI WPI; 1994-242006/30.
DR
XX
XX New glia activating factor polypeptide and antibodies - for use
PT in detection, purification and treatment of diseases, e.g. as
PT anticancer or platelet-increasing agents.
XX
XX Disclosure; Page 43-44; 80pp; English.
XX
XX The glia activating factor (GAF) polypeptides (See AAR56503-56511) can
CC be used as platelet increasing agents, osteogenesis promoting
CC agents or for treating cerebral nervous diseases or hepatopathy such
CC as hepatic cirrhosis. They can also be used to treat cancer when the
CC used alongside an anticancer agent. Antibodies directed against the
CC GAF polypeptides can be used for detecting or determining a
CC biological activity of a GAF polypeptide or for purifying a GAF
CC polypeptide. The antibodies, which also neutralise the cell growth
CC activity of GAF, can be used as anticancer agents.
XX
XX Sequence 175 AA;
SQ
Query Match 9.0%; Score 19; DB 15; Length 175;
Best Local Similarity 100.0%; Pred. No. 9e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 104 AVGLVSIKGVDSGLYLGMN 122
DB 68 AVGLVSIKGVDSGLYLGMN 86
|||||
RESULT 11
AAR56509
ID AAR56509 standard; peptide; 176 AA.
XX
XX AAR56509;
AC
XX
XX 06-MAR-1995 (first entry)
DT
XX
XX Glia activating factor (GAF) peptide.
DE
XX
XX Glia activating factor; GAF; testing; detection; antibody; cancer;
KW osteogenesis; platelet; hepatopathy; cirrhosis; anticancer agent.
KW
XX
XX Homo sapiens.
OS
XX
XX EP608546-A.
PN
XX
XX 03-AUG-1994.
PD
XX
XX 18-DEC-1993; 93EP-0120491.
PF
XX

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PR 22-DEC-1992; 92JP-0342100.
XX 23-AUG-1993; 93JP-0207719.
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Kurokawa T, Kuroshima K, Seko C, Yoshitomi S;
XX WPI; 1994-242006/30.
DR
XX
XX New glia activating factor polypeptide and antibodies - for use
PT in detection, purification and treatment of diseases, e.g. as
PT anticancer or platelet-increasing agents.
XX
XX Disclosure; Page 44; 80pp; English.
XX
XX The glia activating factor (GAF) polypeptides (See AAR56503-56511) can
CC be used as platelet increasing agents, osteogenesis promoting
CC agents or for treating cerebral nervous diseases or hepatopathy such
CC as hepatic cirrhosis. They can also be used to treat cancer when the
CC used alongside an anticancer agent. Antibodies directed against the
CC GAF polypeptides can be used for detecting or determining a
CC biological activity of a GAF polypeptide or for purifying a GAF
CC polypeptide. The antibodies, which also neutralise the cell growth
CC activity of GAF, can be used as anticancer agents.
XX
XX Sequence 176 AA;
SQ
Query Match 9.0%; Score 19; DB 15; Length 176;
Best Local Similarity 100.0%; Pred. No. 9e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 104 AVGLVSIKGVDSGLYLGMN 122
DB 69 AVGLVSIKGVDSGLYLGMN 87
|||||
RESULT 12
AAR27208
ID AAR27208 standard; Protein; 177 AA.
XX
XX AAR27208;
AC
XX
XX 20-MAY-1998 (first entry)
DT
XX
XX Glia activating factor #2.
DE
XX
XX GAF; stimulates glial cell growth; cerebral nerve cell lesions;
KW cerebral oedema; alzheimers disease; senile dementia;
KW diabetic neuropathy; stimulates fibroblasts; burns; wounds; ulcers;
KW stimulates megakaryocytes; increase platelets; haematopoietic cells;
KW immunocompetent cells; vascular smooth muscle cells; bone fractures;
KW osteogenesis promoting activity; osteoporosis; cerebral tumours;
KW stimulates cultured cells.
XX
XX Homo sapiens.
OS
XX
XX EP503297-A.
PN
XX
XX 16-SEP-1992.
PD
XX
XX 13-FEB-1992; 92EP-0102385.
PF
XX
XX 14-FEB-1991; 91JP-0020860.
PR
XX
XX 04-SEP-1991; 91JP-0224454.
PR
XX
XX 10-JAN-1992; 92JP-0003399.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
PA
XX
XX Kondo T, Kurokawa T, Naruo K, Seko C;
PI WPI; 1992-309482/38.
XX
XX N-PSDB; AAQ28411.
DR
XX

```

PT Glia activating factor and its DNA - specifically promotes growth
 PT of glial cells, for treating e.g. cerebral lesions, Alzheimer's
 PT disease, diabetic neuropathies, etc., also in diagnosis
 XX
 PS Claim 1; Fig 19; 87pp; English.
 CC This sequence represents a glia activating factor. It stimulates the
 CC growth of glia cells and can be used to accelerate healing of cerebral
 CC lesions or treat cerebral oedema, alzheimers disease, senile dementia,
 CC or diabetic neuropathy. It also stimulates fibroblasts (for accelerating
 CC healing of burns, wounds, ulcers, etc) megakaryocytes (to increase the
 CC no. of platelets), haematopoietic, immunocompetent and vascular smooth
 CC muscle cells. It is also expected to have osteogenesis-promoting activity
 CC (for treating bone fractures and osteoporosis) Assay of this factor may
 CC be useful in diagnosis of cerebral tumours, and antibodies against could
 CC be used to treat such tumours. It can also be used as a reagent for
 CC stimulating growth of cultured cells. Dosage is 1ng-0.1mg/kg/day.
 XX
 SQ Sequence 177 AA;

Query Match 9.0%; Score 19; DB 13; Length 177;
 Best Local Similarity 100.0%; Pred. No. 9.1e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 104 AVGLVSRGVDSGLYLGMN 122
 |||||
 Db 70 AVGLVSRGVDSGLYLGMN 88

RESULT 13
 AAR27210
 ID AAR27210 standard; Protein; 178 AA.
 AC
 AC AAR27210;
 XX
 DT 20-MAY-1998 (first entry)
 XX
 DE Glia activating factor #4.
 XX
 KW GAF; stimulates glial cell growth; cerebral nerve cell lesions;
 KW cerebral oedema; alzheimers disease; senile dementia;
 KW diabetic neuropathy; stimulates fibroblasts; burns; wounds; ulcers;
 KW stimulates megakaryocytes; increase platelets; haematopoietic cells;
 KW immunocompetent cells; vascular smooth muscle cells; bone fractures;
 KW osteogenesis promoting activity; osteoporosis; cerebral tumours;
 KW stimulates cultured cells.

XX Homo sapiens.
 OS
 XX
 XX EP503297-A.
 XX
 PD 16-SEP-1992.
 XX
 XX 13-FEB-1992; 92EP-0102385.
 XX
 XX 14-FEB-1991; 91JP-0020860.
 PR
 PR 04-SEP-1991; 91JP-0224454.
 PR 10-JAN-1992; 92JP-0003399.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 XX Kondo T, Kurokawa T, Naruo K, Seko C;
 XX
 XX WPI; 1992-309482/38.
 DR
 XX
 XX Glia activating factor and its DNA - specifically promotes growth
 PT of glial cells, for treating e.g. cerebral lesions, Alzheimer's
 PT disease, diabetic neuropathies, etc., also in diagnosis
 XX
 XX Claim 1; Pg5; 7pp; English.

XX This sequence represents a glia activating factor. It stimulates the
 CC growth of glia cells and can be used to accelerate healing of cerebral

CC lesions or treat cerebral oedema, alzheimers disease, senile dementia,
 CC or diabetic neuropathy. It also stimulates fibroblasts (for accelerating
 CC healing of burns, wounds, ulcers, etc) megakaryocytes (to increase the
 CC no. of platelets), haematopoietic, immunocompetent and vascular smooth
 CC muscle cells. It is also expected to have osteogenesis-promoting activity
 CC (for treating bone fractures and osteoporosis) Assay of this factor may
 CC be useful in diagnosis of cerebral tumours, and antibodies against could
 CC be used to treat such tumours. It can also be used as a reagent for
 CC stimulating growth of cultured cells. Dosage is 1ng-0.1mg/kg/day.
 XX
 SQ Sequence 178 AA;

Query Match 9.0%; Score 19; DB 13; Length 178;
 Best Local Similarity 100.0%; Pred. No. 9.1e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 104 AVGLVSRGVDSGLYLGMN 122
 |||||
 Db 71 AVGLVSRGVDSGLYLGMN 89

RESULT 14
 AAR27209
 ID AAR27209 standard; Protein; 205 AA.
 AC
 AC AAR27209;
 XX
 DT 20-MAY-1998 (first entry)
 XX
 DE Glia activating factor #3.
 XX
 KW GAF; stimulates glial cell growth; cerebral nerve cell lesions;
 KW cerebral oedema; alzheimers disease; senile dementia;
 KW diabetic neuropathy; stimulates fibroblasts; burns; wounds; ulcers;
 KW stimulates megakaryocytes; increase platelets; haematopoietic cells;
 KW immunocompetent cells; vascular smooth muscle cells; bone fractures;
 KW osteogenesis promoting activity; osteoporosis; cerebral tumours;
 KW stimulates cultured cells.

XX Homo sapiens.
 OS
 XX
 XX EP503297-A.
 XX
 PD 16-SEP-1992.
 XX
 XX 13-FEB-1992; 92EP-0102385.
 XX
 XX 14-FEB-1991; 91JP-0020860.
 PR
 PR 04-SEP-1991; 91JP-0224454.
 PR 10-JAN-1992; 92JP-0003399.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 XX Kondo T, Kurokawa T, Naruo K, Seko C;
 XX
 XX WPI; 1992-309482/38.
 DR
 XX
 XX Glia activating factor and its DNA - specifically promotes growth
 PT of glial cells, for treating e.g. cerebral lesions, Alzheimer's
 PT disease, diabetic neuropathies, etc., also in diagnosis
 XX
 XX Claim 1; Pg5; 7pp; English.

XX This sequence represents a glia activating factor. It stimulates the
 CC growth of glia cells and can be used to accelerate healing of cerebral
 CC lesions or treat cerebral oedema, alzheimers disease, senile dementia,
 CC or diabetic neuropathy. It also stimulates fibroblasts (for accelerating
 CC healing of burns, wounds, ulcers, etc) megakaryocytes (to increase the
 CC no. of platelets), haematopoietic, immunocompetent and vascular smooth
 CC muscle cells. It is also expected to have osteogenesis-promoting activity
 CC (for treating bone fractures and osteoporosis) Assay of this factor may
 CC be useful in diagnosis of cerebral tumours, and antibodies against could
 CC be used to treat such tumours. It can also be used as a reagent for

CC stimulating growth of cultured cells. Dosage is lng-0.1mg/kg/day.
XX
SQ Sequence 205 AA;
Query Match 9.0%; Score 19; DB 13; Length 205;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 104 AVGLVSIRGVDSGLYLGMN 122
|||||
DB 98 AVGLVSIRGVDSGLYLGMN 116
|||||
RESULT 15
AAR56506
ID AAR56506 standard; peptide; 205 AA.
XX
AC AAR56506;
XX
DT 06-MAR-1995 (first entry)
XX
DE Glia activating factor (GAF) peptide.
XX
KW Glia activating factor; GAF; testing; detection; antibody; cancer;
KW osteogenesis; platelet; hepatopathy; cirrhosis; anticancer agent.
XX
OS Homo sapiens.
XX
PN EP608546-A.
XX
PD 03-AUG-1994.
XX
PF 18-DEC-1993; 93EP-0120491.
XX
PR 22-DEC-1992; 92JP-0342100.
PR 23-AUG-1993; 93JP-0207719.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Kurokawa T, Kuroshima K, Seko C, Yoshitomi S;
XX
DR WPI; 1994-242006/30.
XX
PT New glia activating factor polypeptide and antibodies - for use
PT in detection, purification and treatment of diseases, e.g. as
PT anticancer or platelet-increasing agents.
XX
PS Disclosure; page 41-42; 80pp; English.
XX
CC The glia activating factor (GAF) polypeptides (See AAR56503-56511) can
CC be used as platelet increasing agents, osteogenesis promoting
CC agents or for treating cerebral nervous diseases or hepatopathy such
CC as hepatic cirrhosis. They can also be used to treat cancer when
CC used alongside an anticancer agent. Antibodies directed against the
CC GAF polypeptides can be used for detecting or determining a
CC biological activity of a GAF polypeptide or for purifying a GAF
CC polypeptide. The antibodies, which also neutralise the cell growth
CC activity of GAF, can be used as anticancer agents.
XX
SQ Sequence 205 AA;
Query Match 9.0%; Score 19; DB 15; Length 205;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 104 AVGLVSIRGVDSGLYLGMN 122
|||||
DB 98 AVGLVSIRGVDSGLYLGMN 116
|||||

Search completed: October 21, 2002, 16:19:55
Job time : 70 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 21, 2002, 16:18:46 ; Search time 13 Seconds
(without alignments)
396.446 Million cell updates/sec

Title: US-09-817-814-2

Perfect score: 211

Sequence: 1 MAPLAEGVGLGGLGQQ.....PRVDPERVELYKDLLMYT 211

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Word size : 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /cgn2.6/ptodata/1/1aa/5A-COMB.pep:*
2: /cgn2.6/ptodata/1/1aa/5B-COMB.pep:*
3: /cgn2.6/ptodata/1/1aa/6A-COMB.pep:*
4: /cgn2.6/ptodata/1/1aa/6B-COMB.pep:*
5: /cgn2.6/ptodata/1/1aa/6C-COMB.pep:*
6: /cgn2.6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	9.0	142	1	US-08-340-820-1
2	19	9.0	142	1	US-08-172-328-1
3	19	9.0	142	1	US-08-593-535-1
4	19	9.0	159	1	US-08-172-328-8
5	19	9.0	160	1	US-08-172-328-9
6	19	9.0	175	1	US-08-172-328-6
7	19	9.0	176	1	US-08-172-328-7
8	19	9.0	177	1	US-08-340-820-4
9	19	9.0	177	1	US-08-593-535-4
10	19	9.0	178	1	US-08-340-820-6
11	19	9.0	178	1	US-08-441-629-16
12	19	9.0	190	1	US-08-776-207-16
13	19	9.0	190	3	PCT-US95-09172-16
14	19	9.0	190	5	PCT-US95-09172-16
15	19	9.0	193	2	US-08-438-439C-21
16	19	9.0	205	1	US-08-340-820-5
17	19	9.0	205	1	US-08-172-328-4
18	19	9.0	206	1	US-08-593-535-5
19	19	9.0	206	1	US-08-340-820-7
20	19	9.0	206	1	US-08-340-820-8
21	19	9.0	206	1	US-08-172-328-5
22	19	9.0	206	1	US-08-593-535-7
23	19	9.0	206	1	US-08-340-820-2
24	19	9.0	207	1	US-08-340-820-3
25	19	9.0	207	1	US-08-172-328-2
26	19	9.0	207	1	US-08-593-535-2
27	19	9.0	208	1	US-08-340-820-3

28	19	9.0	208	1	US-08-340-820-9	Sequence 9, Appli
29	19	9.0	208	1	US-08-340-820-25	Sequence 25, Appli
30	19	9.0	208	1	US-08-172-328-3	Sequence 3, Appli
31	19	9.0	208	1	US-08-593-535-3	Sequence 3, Appli
32	19	9.0	208	1	US-08-593-535-9	Sequence 9, Appli
33	19	9.0	208	1	US-08-593-535-25	Sequence 25, Appli
34	19	9.0	208	1	US-08-439-725A-7	Sequence 7, Appli
35	19	9.0	208	1	US-08-464-590A-10	Sequence 10, Appli
36	19	9.0	208	1	US-08-462-169B-17	Sequence 17, Appli
37	19	9.0	208	2	US-08-207-412B-13	Sequence 13, Appli
38	19	9.0	208	2	US-08-867-471-7	Sequence 7, Appli
39	19	9.0	208	2	US-08-438-439C-12	Sequence 12, Appli
40	19	9.0	208	2	US-08-951-822-34	Sequence 34, Appli
41	19	9.0	208	2	US-08-943-915-3	Sequence 3, Appli
42	19	9.0	208	3	US-09-103-079-17	Sequence 17, Appli
43	19	9.0	208	3	US-08-705-245-7	Sequence 7, Appli
44	19	9.0	208	3	US-08-718-904-18	Sequence 18, Appli
45	19	9.0	208	3	US-09-023-082A-18	Sequence 18, Appli
46	19	9.0	208	3	US-09-093-585-10	Sequence 10, Appli
47	19	9.0	208	4	US-09-368-951-34	Sequence 34, Appli
48	16	7.6	173	2	US-08-943-915-32	Sequence 32, Appli
49	16	7.6	198	2	US-08-943-915-33	Sequence 33, Appli
50	16	7.6	207	2	US-08-943-915-2	Sequence 2, Appli
51	16	7.6	207	2	US-08-943-915-5	Sequence 5, Appli
52	10	4.7	155	1	US-08-462-169B-24	Sequence 24, Appli
53	10	4.7	155	3	US-09-103-079-24	Sequence 24, Appli
54	10	4.7	158	3	US-08-776-207-18	Sequence 18, Appli
55	9	4.3	27	1	US-08-290-373B-10	Sequence 10, Appli
56	7	3.3	114	4	US-09-199-637A-257	Sequence 257, App
57	7	3.3	424	2	US-08-592-214A-16	Sequence 16, Appli
58	7	3.3	424	3	US-08-659-188-16	Sequence 16, Appli
59	7	3.3	424	3	US-08-655-227-16	Sequence 16, Appli
60	7	3.3	424	3	US-08-655-241-16	Sequence 16, Appli
61	7	3.3	424	3	US-09-149-976-16	Sequence 16, Appli
62	7	3.3	424	4	US-09-398-326-16	Sequence 16, Appli
63	7	3.3	694	3	US-08-724-586-2	Sequence 2, Appli
64	7	3.3	694	4	US-09-421-632-2	Sequence 2, Appli
65	7	3.3	705	2	US-08-655-840-2	Sequence 2, Appli
66	7	3.3	708	2	US-08-655-840-4	Sequence 4, Appli
67	7	3.3	709	1	US-08-154-019-2	Sequence 2, Appli
68	7	3.3	709	1	US-08-461-333-2	Sequence 2, Appli
69	7	3.3	709	3	US-08-464-167-2	Sequence 2, Appli
70	7	3.3	709	3	US-09-158-313-2	Sequence 2, Appli
71	7	3.3	709	4	US-08-476-798-2	Sequence 2, Appli
72	7	3.3	711	1	US-08-145-681-2	Sequence 2, Appli
73	7	3.3	711	1	US-08-250-308-2	Sequence 2, Appli
74	7	3.3	711	1	US-08-154-019-4	Sequence 4, Appli
75	7	3.3	711	1	US-08-461-333-4	Sequence 4, Appli
76	7	3.3	711	1	US-08-453-703-2	Sequence 2, Appli
77	7	3.3	711	2	US-08-456-106-2	Sequence 2, Appli
78	7	3.3	711	3	US-08-464-167-4	Sequence 4, Appli
79	7	3.3	711	3	US-09-158-313-4	Sequence 4, Appli
80	7	3.3	711	3	US-08-456-108-2	Sequence 2, Appli
81	7	3.3	711	4	US-08-476-798-4	Sequence 4, Appli
82	7	3.3	711	4	US-09-265-577-2	Sequence 2, Appli
83	7	3.3	711	5	PCT-US93-03614-2	Sequence 2, Appli
84	7	3.3	853	4	US-09-354-129-10	Sequence 10, Appli
85	7	3.3	4302	3	US-08-658-136-5	Sequence 5, Appli
86	7	3.3	4303	2	US-08-460-751-2	Sequence 2, Appli
87	6	2.8	8	2	US-08-249-830-11	Sequence 11, Appli
88	6	2.8	8	2	US-08-645-193B-44	Sequence 44, Appli
89	6	2.8	8	3	US-09-198-209-11	Sequence 11, Appli
90	6	2.8	10	2	US-08-758-307B-1	Sequence 1, Appli
91	6	2.8	10	4	US-08-977-378-8	Sequence 8, Appli
92	6	2.8	11	4	US-08-977-378-7	Sequence 7, Appli
93	6	2.8	11	4	US-08-977-378-15	Sequence 15, Appli
94	6	2.8	11	4	US-08-977-378-16	Sequence 16, Appli
95	6	2.8	11	4	US-08-977-378-23	Sequence 23, Appli
96	6	2.8	15	4	US-08-977-378-27	Sequence 27, Appli
97	6	2.8	20	1	US-08-524-677-2	Sequence 2, Appli
98	6	2.8	40	1	US-08-145-708A-17	Sequence 17, Appli
99	6	2.8	40	2	US-08-331-454-17	Sequence 17, Appli
100	6	2.8	42	1	US-08-450-945-61	Sequence 61, Appli

101	6	2.8	42	4	US-08-976-161-61	Sequence 61, Appl	174	6	2.8	208	1	US-08-551-171-6	Sequence 6, Appl
102	6	2.8	50	3	US-08-630-916A-121	Sequence 121, App	175	6	2.8	208	1	US-08-464-590A-16	Sequence 16, Appl
103	6	2.8	68	1	US-08-524-677-1	Sequence 1, Appl	176	6	2.8	208	1	US-08-462-169B-14	Sequence 14, Appl
104	6	2.8	83	2	US-08-417-210A-96	Sequence 96, Appl	177	6	2.8	208	2	US-08-207-412B-11	Sequence 11, Appl
105	6	2.8	95	1	US-08-202-389-21	Sequence 21, Appl	178	6	2.8	208	2	US-08-951-822-27	Sequence 27, Appl
106	6	2.8	95	1	US-08-202-389-22	Sequence 22, Appl	179	6	2.8	208	3	US-09-103-079-14	Sequence 14, Appl
107	6	2.8	106	1	US-07-732-242C-2	Sequence 2, Appl	180	6	2.8	208	3	US-08-902-233-6	Sequence 6, Appl
108	6	2.8	107	1	US-08-015-986A-4	Sequence 4, Appl	181	6	2.8	208	3	US-09-093-585-16	Sequence 16, Appl
109	6	2.8	107	2	US-08-015-986A-5	Sequence 5, Appl	182	6	2.8	208	3	US-09-368-951-27	Sequence 27, Appl
110	6	2.8	107	2	US-08-446-363-4	Sequence 4, Appl	183	6	2.8	219	1	US-08-441-629-13	Sequence 13, Appl
111	6	2.8	107	2	US-08-446-363-5	Sequence 5, Appl	184	6	2.8	219	3	US-08-776-207-13	Sequence 13, Appl
112	6	2.8	114	4	US-09-183-959-14	Sequence 14, Appl	185	6	2.8	219	5	PCT-US95-09172-13	Sequence 13, Appl
113	6	2.8	121	4	US-08-822-573-4	Sequence 4, Appl	186	6	2.8	231	3	US-08-908-332-6	Sequence 6, Appl
114	6	2.8	122	6	5304466-3	Patent No. 5304466	187	6	2.8	236	4	US-09-230-196-22	Sequence 22, Appl
115	6	2.8	123	6	US-08-822-573-2	Sequence 2, Appl	188	6	2.8	237	2	US-08-467-822-20	Sequence 20, Appl
116	6	2.8	123	4	US-09-124-900-10	Sequence 10, Appl	189	6	2.8	237	4	US-08-432-697-20	Sequence 20, Appl
117	6	2.8	129	4	US-09-135-994-12	Sequence 12, Appl	190	6	2.8	237	4	US-08-466-248-20	Sequence 20, Appl
118	6	2.8	140	1	US-08-187-780-1	Sequence 1, Appl	191	6	2.8	238	4	US-09-605-858-35	Sequence 35, Appl
119	6	2.8	140	2	US-08-478-485-1	Sequence 1, Appl	192	6	2.8	239	4	US-08-679-493A-76	Sequence 76, Appl
120	6	2.8	145	1	US-08-551-171-3	Sequence 3, Appl	193	6	2.8	245	2	US-08-685-992-26	Sequence 26, Appl
121	6	2.8	145	3	US-08-902-233-3	Sequence 3, Appl	194	6	2.8	245	2	US-09-144-925-26	Sequence 26, Appl
122	6	2.8	146	1	US-08-551-171-4	Sequence 4, Appl	195	6	2.8	266	3	US-08-815-809-5	Sequence 5, Appl
123	6	2.8	146	3	US-08-902-233-4	Sequence 4, Appl	196	6	2.8	266	6	5175383-5	Patent No. 5175383
124	6	2.8	148	1	US-08-102-691-3	Sequence 3, Appl	197	6	2.8	267	1	US-08-462-169B-13	Sequence 13, Appl
125	6	2.8	161	2	US-08-286-819A-25	Sequence 25, Appl	198	6	2.8	267	3	US-09-103-079-13	Sequence 13, Appl
126	6	2.8	161	3	US-08-980-357-25	Sequence 25, Appl	199	6	2.8	268	1	US-08-439-750A-12	Sequence 12, Appl
127	6	2.8	170	1	US-08-551-171-1	Sequence 1, Appl	200	6	2.8	268	1	US-08-464-590A-17	Sequence 17, Appl
128	6	2.8	170	3	US-08-902-233-1	Sequence 1, Appl	201	6	2.8	268	2	US-08-207-412B-12	Sequence 12, Appl
129	6	2.8	171	1	US-08-551-171-2	Sequence 2, Appl	202	6	2.8	268	2	US-08-867-471-12	Sequence 12, Appl
130	6	2.8	171	3	US-08-902-233-2	Sequence 2, Appl	203	6	2.8	268	2	US-08-438-439C-8	Sequence 8, Appl
131	6	2.8	174	1	US-08-551-171-7	Sequence 7, Appl	204	6	2.8	268	2	US-08-951-822-33	Sequence 33, Appl
132	6	2.8	174	3	US-08-902-233-7	Sequence 7, Appl	205	6	2.8	268	3	US-08-705-745-14	Sequence 14, Appl
133	6	2.8	175	1	US-08-102-691-2	Sequence 2, Appl	206	6	2.8	268	3	US-08-718-904-14	Sequence 14, Appl
134	6	2.8	175	1	US-08-551-171-8	Sequence 8, Appl	207	6	2.8	268	3	US-09-023-082A-15	Sequence 15, Appl
135	6	2.8	175	3	US-08-902-233-8	Sequence 8, Appl	208	6	2.8	268	4	US-09-093-585-17	Sequence 17, Appl
136	6	2.8	177	6	5430019-2	Patent No. 5430019	209	6	2.8	268	4	US-09-368-951-33	Sequence 33, Appl
137	6	2.8	187	1	US-08-441-629-11	Sequence 11, Appl	210	6	2.8	269	2	US-08-438-439C-18	Sequence 18, Appl
138	6	2.8	187	3	US-08-776-207-11	Sequence 11, Appl	211	6	2.8	275	4	US-09-036-987A-27	Sequence 27, Appl
139	6	2.8	187	5	PCT-US95-09172-11	Sequence 11, Appl	212	6	2.8	275	4	US-09-370-700-27	Sequence 27, Appl
140	6	2.8	198	1	US-08-439-725A-14	Sequence 14, Appl	213	6	2.8	280	2	US-08-816-155B-43	Sequence 43, Appl
141	6	2.8	198	1	US-08-441-629-12	Sequence 12, Appl	214	6	2.8	280	4	US-09-079-587-43	Sequence 43, Appl
142	6	2.8	198	2	US-08-867-471-14	Sequence 14, Appl	215	6	2.8	317	2	US-08-555-722-8	Sequence 8, Appl
143	6	2.8	198	2	US-08-438-439C-10	Sequence 10, Appl	216	6	2.8	317	3	US-08-911-853-25	Sequence 25, Appl
144	6	2.8	198	2	US-08-438-439C-20	Sequence 20, Appl	217	6	2.8	317	4	US-09-479-409-25	Sequence 25, Appl
145	6	2.8	198	3	US-08-705-245-15	Sequence 15, Appl	218	6	2.8	317	4	US-09-384-301-8	Sequence 8, Appl
146	6	2.8	198	3	US-08-718-904-15	Sequence 15, Appl	219	6	2.8	317	4	US-09-479-453-25	Sequence 25, Appl
147	6	2.8	198	3	US-09-023-082A-14	Sequence 14, Appl	220	6	2.8	319	4	US-08-836-075A-48	Sequence 48, Appl
148	6	2.8	198	3	US-08-776-207-12	Sequence 12, Appl	221	6	2.8	345	4	US-09-232-191-3	Sequence 3, Appl
149	6	2.8	198	5	PCT-US95-09172-12	Sequence 12, Appl	222	6	2.8	345	4	US-09-232-200-3	Sequence 3, Appl
150	6	2.8	202	4	US-09-026-958-2	Sequence 2, Appl	223	6	2.8	345	4	US-09-232-197-3	Sequence 3, Appl
151	6	2.8	202	4	US-09-057-860A-2	Sequence 2, Appl	224	6	2.8	345	4	US-09-232-201-3	Sequence 3, Appl
152	6	2.8	205	6	5175383-6	Patent No. 5175383	225	6	2.8	347	1	US-08-842-540-2	Sequence 2, Appl
153	6	2.8	206	1	US-08-102-691-1	Sequence 1, Appl	226	6	2.8	347	1	US-08-690-413-2	Sequence 2, Appl
154	6	2.8	206	1	US-08-439-725A-13	Sequence 13, Appl	227	6	2.8	349	4	US-09-343-001B-1	Sequence 1, Appl
155	6	2.8	206	1	US-08-464-590A-15	Sequence 15, Appl	228	6	2.8	350	4	US-09-157-603-3	Sequence 3, Appl
156	6	2.8	206	1	US-08-441-629-10	Sequence 10, Appl	229	6	2.8	350	4	US-09-587-436-3	Sequence 3, Appl
157	6	2.8	206	1	US-08-462-169B-12	Sequence 12, Appl	230	6	2.8	353	4	US-08-838-151A-44	Sequence 44, Appl
158	6	2.8	206	2	US-08-207-412B-10	Sequence 10, Appl	231	6	2.8	353	4	US-08-838-151A-46	Sequence 46, Appl
159	6	2.8	206	2	US-08-867-471-9	Sequence 9, Appl	232	6	2.8	353	4	US-08-838-151A-49	Sequence 49, Appl
160	6	2.8	206	2	US-08-438-439C-9	Sequence 9, Appl	233	6	2.8	353	4	US-08-838-151A-52	Sequence 52, Appl
161	6	2.8	206	2	US-08-951-822-26	Sequence 26, Appl	234	6	2.8	353	4	US-08-838-151A-55	Sequence 55, Appl
162	6	2.8	206	3	US-08-388-353-644	Sequence 644, App	235	6	2.8	357	4	US-08-838-151A-20	Sequence 20, Appl
163	6	2.8	206	3	US-09-103-079-12	Sequence 12, Appl	236	6	2.8	357	4	US-08-838-151A-24	Sequence 24, Appl
164	6	2.8	206	3	US-08-488-551B-644	Sequence 644, App	237	6	2.8	357	4	US-08-838-151A-27	Sequence 27, Appl
165	6	2.8	206	3	US-08-705-245-13	Sequence 13, Appl	238	6	2.8	358	1	US-08-239-431A-30	Sequence 30, Appl
166	6	2.8	206	3	US-08-718-904-13	Sequence 13, Appl	239	6	2.8	358	1	US-08-239-431A-4	Sequence 4, Appl
167	6	2.8	206	3	US-09-023-082A-13	Sequence 13, Appl	240	6	2.8	358	2	US-08-463-081B-6	Sequence 6, Appl
168	6	2.8	206	3	US-08-776-207-10	Sequence 10, Appl	241	6	2.8	358	2	US-08-461-379A-6	Sequence 6, Appl
169	6	2.8	206	3	US-09-093-585-15	Sequence 15, Appl	242	6	2.8	358	2	US-08-462-390B-6	Sequence 6, Appl
170	6	2.8	206	4	US-09-368-951-26	Sequence 26, Appl	243	6	2.8	358	3	US-08-463-074B-6	Sequence 6, Appl
171	6	2.8	207	5	PCT-US95-09172-10	Sequence 10, Appl	244	6	2.8	358	3	US-08-465-585C-6	Sequence 6, Appl
172	6	2.8	207	1	US-08-551-171-5	Sequence 5, Appl	245	6	2.8	358	3	US-08-652-446-6	Sequence 6, Appl
173	6	2.8	207	3	US-08-902-233-5	Sequence 5, Appl	246	6	2.8	359	4	US-08-809-103B-2	Sequence 2, Appl

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248	6	2.8	359	4	US-08-809-103B-6	Sequence 6, Appli	321	6	2.8	758	4	US-09-413-814-32	Sequence 32, Appli
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260	6	2.8	447	4	US-09-370-253-2	Sequence 2, Appli	333	6	2.8	814	4	US-09-417-381A-3	Sequence 3, Appli
261	6	2.8	450	2	US-08-665-037-2	Sequence 2, Appli	334	6	2.8	830	3	US-08-872-855-11	Sequence 11, Appli
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263	6	2.8	450	2	US-08-732-870-2	Sequence 2, Appli	336	6	2.8	833	1	US-08-264-534-6	Sequence 6, Appli
264	6	2.8	461	1	US-07-796-361A-13	Sequence 13, Appli	337	6	2.8	833	1	US-08-083-590A-2	Sequence 2, Appli
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266	6	2.8	462	1	US-07-612-673-4	Sequence 4, Appli	339	6	2.8	833	2	US-08-346-126-6	Sequence 6, Appli
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270	6	2.8	483	3	US-08-369-822C-22	Sequence 22, Appli	343	6	2.8	834	4	US-09-143-571-29	Sequence 29, Appli
271	6	2.8	483	3	US-08-582-776C-37	Sequence 37, Appli	344	6	2.8	922	2	US-08-464-402-2	Sequence 2, Appli
272	6	2.8	483	3	US-08-434-831B-34	Sequence 34, Appli	345	6	2.8	922	4	US-09-054-775C-2	Sequence 2, Appli
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274	6	2.8	484	3	US-08-582-776C-36	Sequence 36, Appli	347	6	2.8	941	4	US-09-074-658-75	Sequence 75, Appli
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283	6	2.8	591	3	US-09-082-737-2	Sequence 2, Appli	356	6	2.8	1049	2	US-08-817-090B-2	Sequence 2, Appli
284	6	2.8	607	3	US-08-537-361B-10	Sequence 10, Appli	357	6	2.8	1057	3	US-08-931-820-4	Sequence 4, Appli
285	6	2.8	607	3	US-08-990-470A-4	Sequence 4, Appli	358	6	2.8	1078	3	US-08-963-825-21	Sequence 21, Appli
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291	6	2.8	618	1	US-08-468-852-10	Sequence 10, Appli	364	6	2.8	1430	4	US-09-210-361-6	Sequence 6, Appli
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293	6	2.8	621	2	US-08-419-652-4	Sequence 4, Appli	366	6	2.8	1501	2	US-08-716-679-3	Sequence 3, Appli
294	6	2.8	635	2	US-08-484-101B-36	Sequence 36, Appli	367	6	2.8	1732	2	US-08-570-311-10	Sequence 10, Appli
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298	6	2.8	650	4	US-09-232-191-29	Sequence 29, Appli	371	6	2.8	1911	2	US-08-800-825A-5	Sequence 5, Appli
299	6	2.8	650	4	US-09-232-200-79	Sequence 79, Appli	372	6	2.8	1911	4	US-09-158-657-5	Sequence 5, Appli
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305	6	2.8	652	1	US-08-050-684-2	Sequence 2, Appli	378	6	2.8	2987	2	US-08-970-269A-29	Sequence 29, Appli
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315	6	2.8	662	2	US-08-685-118-4	Sequence 4, Appli	388	6	2.8	4550	2	US-08-804-227C-8	Sequence 8, Appli
316	6	2.8	662	2	US-08-915-495-4	Sequence 4, Appli	389	6	2.8	4550	2	US-08-804-198-2	Sequence 2, Appli
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318	6	2.8	662	2	US-08-789-350-2	Sequence 2, Appli	391	6	2.4	5	1	US-07-969-307A-8	Sequence 8, Appli
319	6	2.8	679	4	US-09-056-556-194	Sequence 194, App	392	6	2.4	5	1	US-08-257-782-18	Sequence 18, Appli

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395	5	2.4	5	2	US-08-079-144-18	Sequence 18, Appl	468	18	3	US-08-928-694-38	Sequence 38, Appl
396	5	2.4	5	5	PCT-US94-026311-95	Sequence 95, Appl	469	18	5	PCT-US91-06950-35	Sequence 35, Appl
397	5	2.4	5	6	US-07-822-924-9	Sequence 9, Appl	470	18	5	PCT-US91-06950-38	Sequence 38, Appl
398	5	2.4	6	1	US-07-969-307A-11	Sequence 11, Appl	471	19	1	US-08-451-947-41	Sequence 41, Appl
399	5	2.4	6	2	US-09-060-455-18	Sequence 18, Appl	472	19	2	US-08-424-826A-41	Sequence 41, Appl
400	5	2.4	6	3	US-08-888-381-9	Sequence 9, Appl	473	19	2	US-08-793-490-5	Sequence 5, Appl
401	5	2.4	6	3	PCT-US93-00683-9	Sequence 9, Appl	474	19	3	US-08-928-694-41	Sequence 41, Appl
402	5	2.4	7	1	US-07-945-982-3	Sequence 3, Appl	475	19	5	PCT-US91-06950-41	Sequence 41, Appl
403	5	2.4	7	1	US-07-969-307A-14	Sequence 14, Appl	476	20	1	US-07-686-116A-1	Sequence 1, Appl
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405	5	2.4	8	1	US-07-969-307A-17	Sequence 17, Appl	478	20	1	US-07-686-116A-5	Sequence 5, Appl
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407	5	2.4	8	6	5466668-42	Patent No. 5466668	480	20	1	US-07-895-252-7	Sequence 7, Appl
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409	5	2.4	9	1	US-08-215-805A-76	Sequence 76, Appl	482	20	1	US-08-637-759B-459	Sequence 459, App
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411	5	2.4	9	4	US-09-042-107-57	Sequence 57, Appl	484	20	3	US-08-916-913A-6	Sequence 6, Appl
412	5	2.4	9	4	US-09-502-600-76	Sequence 76, Appl	485	20	3	US-08-871-355A-459	Sequence 459, App
413	5	2.4	9	4	US-09-502-600-91	Sequence 91, Appl	486	20	4	US-08-602-999A-109	Sequence 109, App
414	5	2.4	9	4	US-09-518-046-57	Sequence 57, Appl	487	20	4	US-09-247-527-18	Sequence 18, Appl
415	5	2.4	9	4	US-09-518-046-59	Sequence 59, Appl	488	20	4	US-09-439-313-492	Sequence 492, App
416	5	2.4	10	1	US-08-068-947-28	Sequence 28, Appl	489	20	4	US-09-439-313-570	Sequence 570, App
417	5	2.4	10	1	US-08-068-947-30	Sequence 30, Appl	490	20	4	US-09-201-945-429	Sequence 459, App
418	5	2.4	10	1	US-08-068-947-33	Sequence 33, Appl	491	20	4	US-08-630-172-36	Sequence 36, Appl
419	5	2.4	10	1	US-08-068-947-41	Sequence 41, Appl	492	22	3	US-09-375-419-36	Sequence 36, Appl
420	5	2.4	10	1	US-08-222-619-10	Sequence 10, Appl	493	22	3	US-08-086-428B-148	Sequence 148, App
421	5	2.4	10	3	US-09-139-762A-54	Sequence 54, Appl	494	23	1	US-08-251-472-5	Sequence 5, Appl
422	5	2.4	10	3	US-08-836-075A-189	Sequence 189, App	495	23	2	US-08-468-570-148	Sequence 148, App
423	5	2.4	10	4	PCT-US95-04075-10	Sequence 33, Appl	496	23	2	US-08-290-665A-252	Sequence 252, App
424	5	2.4	10	5	US-09-025-596-33	Sequence 33, Appl	497	23	3	US-08-105-904B-10	Sequence 10, Appl
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426	5	2.4	11	1	US-08-068-947-39	Sequence 39, Appl	499	23	4	US-08-114-877A-10	Sequence 10, Appl
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433	5	2.4	13	1	US-08-469-615-8	Sequence 8, Appl	506	24	1	US-08-484-635-125	Sequence 125, App
434	5	2.4	13	1	US-08-466-763-8	Sequence 8, Appl	507	24	2	US-08-484-631-125	Sequence 125, App
435	5	2.4	13	2	US-08-411-142A-8	Sequence 8, Appl	508	24	2	US-08-827-570-125	Sequence 13, Appl
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438	5	2.4	14	1	US-07-791-935B-9	Sequence 9, Appl	511	24	4	US-08-461-697-152	Sequence 8, Appl
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452	5	2.4	17	2	US-08-650-262-14	Sequence 14, Appl	525	27	4	US-09-074-114-9	Sequence 9, Appl
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463	5	2.4	18	2	US-08-471-282A-84	Sequence 84, Appl	536	29	2	US-08-637-418-14	Sequence 14, Appl
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465	5	2.4	18	3	US-08-468-739C-84	Sequence 84, Appl	538	29	2		

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548	5	2.4	30	3	US-08-928-694-43	Sequence 43, Appl	621	5	2.4	51	4	US-09-138-873A-3	Sequence 3, Appl
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550	5	2.4	30	5	PCT-US91-06950-43	Sequence 43, Appl	623	5	2.4	52	1	US-08-479-650-38	Sequence 38, Appl
551	5	2.4	31	2	US-08-508-664-8	Sequence 8, Appl	624	5	2.4	52	1	US-08-191-866D-60	Sequence 60, Appl
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555	5	2.4	32	1	US-08-158-189-22	Sequence 22, Appl	628	5	2.4	53	1	US-08-014-153D-51	Sequence 51, Appl
556	5	2.4	32	2	US-08-491-204A-5	Sequence 5, Appl	629	5	2.4	53	1	US-08-014-153D-52	Sequence 52, Appl
557	5	2.4	32	2	US-08-598-873-22	Sequence 22, Appl	630	5	2.4	53	1	US-08-014-153D-53	Sequence 53, Appl
558	5	2.4	32	3	US-08-938-548B-7	Sequence 7, Appl	631	5	2.4	53	1	US-08-014-153D-54	Sequence 54, Appl
559	5	2.4	32	3	US-08-484-322-63	Sequence 63, Appl	632	5	2.4	54	1	US-08-757-541-8	Sequence 8, Appl
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564	5	2.4	32	4	US-09-240-078-5	Sequence 5, Appl	637	5	2.4	54	2	US-08-660-963-18	Sequence 18, Appl
565	5	2.4	32	4	US-08-939-093A-7	Sequence 7, Appl	638	5	2.4	54	3	US-08-630-916A-118	Sequence 118, App
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581	5	2.4	35	2	US-09-134-836-3	Sequence 3, Appl	654	5	2.4	58	2	US-08-928-694-42	Sequence 42, Appl
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ALIGNMENTS

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RESULT 1
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; Patent No. 5512460
; GENERAL INFORMATION:
; APPLICANT: NARUO, Ken-ichi
; APPLICANT: SEKO, Chisako
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KONDO, Tatsuya
; TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND ITS
; TITLE OF INVENTION: PRODUCTION
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,820
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US/07/835,713
; FILING DATE:
; APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G.
; REGISTRATION NUMBER: 27026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 48 AVGLVSIRGVDSGLYGMN 66
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; Sequence 1, Application US/08172328
; Patent No. 5571895
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KUROSHIMA, Ken-ichi
; APPLICANT: YOSHITOMI, Sumie
; APPLICANT: SEKO, Sachiko
; TITLE OF INVENTION: ANTIBODIES, POLYPEPTIDES, PRODUCTION AND
; TITLE OF INVENTION: USE THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/172,328
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: NEUNER, George W.
; REGISTRATION NUMBER: 26964
; REFERENCE/DOCKET NUMBER: 26964
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
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; ORGANISM: Homo sapiens
; HAPLOTYPE: 2n
; TISSUE TYPE: Skin
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; LIBRARY: Human foreskin cdna library
; CLONE: pGAF1
US-08-172-328-1
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RESULT 3
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; Patent No. 5622928
; GENERAL INFORMATION:
; APPLICANT: NARUO, Ken-ichi
; APPLICANT: SEKO, Chisako
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KONDO, Tatsuya
; TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND ITS
; TITLE OF INVENTION: PRODUCTION
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 12-FEB-1992
; APPLICATION NUMBER: US/08/593,535
; FILING DATE: 24-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/835,713
; FILING DATE: 12-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G.
; REGISTRATION NUMBER: 27026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-593-535-1
Query Match 9.0%; Score 19; DB 1; Length 142;
Best Local Similarity 100.0%; Pred. No. 5.5e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 104 AVGLVSRGVDSGLYLGMN 122
Db 48 AVGLVSRGVDSGLYLGMN 66
RESULT 4
US-08-172-328-8
; Sequence 8, Application US/08172328
; Patent No. 5571895
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KUROSHIMA, Ken-ichi
; APPLICANT: YOSHITOMI, Sumie
; APPLICANT: SEKO, Sachiko
; TITLE OF INVENTION: ANTIBODIES, POLYPEPTIDES, PRODUCTION AND
; TITLE OF INVENTION: USE THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 08-08-172,328
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: NEUNER, George W
; REGISTRATION NUMBER: 26964
; REFERENCE/DOCKET NUMBER: 26964
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 159 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; HAPLOTYPE: 2n
; TISSUE TYPE: Skin
; CELL TYPE: Fibroblast
; IMMEDIATE SOURCE:
; LIBRARY: Human foreskin cDNA library
; CLONE: pGAF1
; US-08-172-328-8
Query Match 9.0%; Score 19; DB 1; Length 159;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 104 AVGLVSRGVDSGLYLGMN 122
Db 52 AVGLVSRGVDSGLYLGMN 70
RESULT 5
US-08-172-328-9
; Sequence 9, Application US/08172328
; Patent No. 5571895
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KUROSHIMA, Ken-ichi
; APPLICANT: YOSHITOMI, Sumie
; APPLICANT: SEKO, Sachiko
; TITLE OF INVENTION: ANTIBODIES, POLYPEPTIDES, PRODUCTION AND
; TITLE OF INVENTION: USE THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/172,328
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: NEUNER, George W
; REGISTRATION NUMBER: 26964
; REFERENCE/DOCKET NUMBER: 26964
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 160 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; HAPLOTYPE: 2n
; TISSUE TYPE: Skin
; CELL TYPE: Fibroblast
; IMMEDIATE SOURCE:
; LIBRARY: Human foreskin cdna library
; CLONE: pGAF1
; US-08-172-328-9

Query Match          9.0%; Score 19; DB 1; Length 160;
Best Local Similarity 100.0%; Pred. No. 6.1e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 AVGLVSIKGVDSGLYLGMN 122
Db 53 AVGLVSIKGVDSGLYLGMN 71

RESULT 6
US-08-172-328-6
; Sequence 6, Application US/08172328
; Patent No. 5571895
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KUROSHIMA, Ken-ichi
; APPLICANT: YOSHITOMI, Sumie
; APPLICANT: SEKO, Sachiko
; TITLE OF INVENTION: ANTIBODIES, POLYPEPTIDES, PRODUCTION AND
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/172,328
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: NEUNER, George W
; REGISTRATION NUMBER: 26964
; REFERENCE/DOCKET NUMBER: 26964
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 176 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; US-08-172-328-8

;
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; HAPLOTYPE: 2n
; TISSUE TYPE: Skin
; CELL TYPE: Fibroblast
; IMMEDIATE SOURCE:
; LIBRARY: Human foreskin cdna library
; CLONE: pGAF1
; US-08-172-328-6

Query Match          9.0%; Score 19; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 6.6e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 AVGLVSIKGVDSGLYLGMN 122
Db 68 AVGLVSIKGVDSGLYLGMN 86

RESULT 7
US-08-172-328-7
; Sequence 7, Application US/08172328
; Patent No. 5571895
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KUROSHIMA, Ken-ichi
; APPLICANT: YOSHITOMI, Sumie
; APPLICANT: SEKO, Sachiko
; TITLE OF INVENTION: ANTIBODIES, POLYPEPTIDES, PRODUCTION AND
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/172,328
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: NEUNER, George W
; REGISTRATION NUMBER: 26964
; REFERENCE/DOCKET NUMBER: 26964
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 176 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; US-08-172-328-7
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ORGANISM: Homo sapiens
HAPLOTYPE: 2n
TISSUE TYPE: Skin
CELL TYPE: Fibroblast
IMMEDIATE SOURCE:
LIBRARY: Human foreskin cDNA library
CLONE: pGAF1
US-08-172-328-7

Query Match 9.0%; Score 19; DB 1; Length 176;
Best Local Similarity 100.0%; Pred. No. 6.6e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVSIRGVDSGLYLGMN 122
|||||
Db 69 AVGLVSIRGVDSGLYLGMN 87

RESULT 8
US-08-340-820-4
; Sequence 4, Application US/08340820
; Patent No. 5512460
; GENERAL INFORMATION:
; APPLICANT: NARUO, Ken-ichi
; APPLICANT: SEKO, Chisako
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KONDO, Tatsuya
; TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND ITS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340.820
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/835,713
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G.
; REGISTRATION NUMBER: 27026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-340-820-4

Query Match 9.0%; Score 19; DB 1; Length 177;
Best Local Similarity 100.0%; Pred. No. 6.7e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVSIRGVDSGLYLGMN 122
|||||
Db 70 AVGLVSIRGVDSGLYLGMN 88

RESULT 9
US-08-593-535-4
; Sequence 4, Application US/08593535
; Patent No. 5622928
; GENERAL INFORMATION:
; APPLICANT: NARUO, Ken-ichi
; APPLICANT: SEKO, Chisako
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KONDO, Tatsuya
; TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND ITS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/593,535
; FILING DATE: 24-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/835,713
; FILING DATE: 12-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G.
; REGISTRATION NUMBER: 27026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-593-535-4

Query Match 9.0%; Score 19; DB 1; Length 177;
Best Local Similarity 100.0%; Pred. No. 6.7e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVSIRGVDSGLYLGMN 122
|||||
Db 70 AVGLVSIRGVDSGLYLGMN 88

RESULT 10
US-08-340-820-6
; Sequence 6, Application US/08340820
; Patent No. 5512460
; GENERAL INFORMATION:
; APPLICANT: NARUO, Ken-ichi
; APPLICANT: SEKO, Chisako
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KONDO, Tatsuya
; TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND ITS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street

```

; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,820
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/835,713
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G.
; REGISTRATION NUMBER: 27026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-340-820-6

Query Match          9.0%; Score 19; DB 1; Length 178;
Best Local Similarity 100.0%; Pred. No. 6.7e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVSIRGVDGSLGLGMN 122
Db 71 AVGLVSIRGVDGSLGLGMN 89

RESULT 11
US-08-593-535-6
; Sequence 6, Application US/08593535
; Patent No. 5622928
; GENERAL INFORMATION:
; APPLICANT: NARUO, Ken-ichi
; APPLICANT: SEKO, Chisako
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KONDO, Tatsuya
; TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND ITS
; TITLE OF INVENTION: PRODUCTION
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/593,535
; FILING DATE: 24-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/835,713
; FILING DATE: 12-FEB-1992
; ATTORNEY/AGENT INFORMATION:

; CITY: CONLIN, David G.
; REGISTRATION NUMBER: 27026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-441-629-16

Query Match          9.0%; Score 19; DB 1; Length 178;
Best Local Similarity 100.0%; Pred. No. 6.7e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVSIRGVDGSLGLGMN 122
Db 71 AVGLVSIRGVDGSLGLGMN 89

RESULT 12
US-08-441-629-16
; Sequence 16, Application US/08441629
; Patent No. 5766923
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Marc W.
; APPLICANT: Kinoshita, No. 5766923Iyuki
; TITLE OF INVENTION: RECEPTOR-LIGAND ASSAY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,629
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/279,217
; FILING DATE: 22-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: H095-01A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 190 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-441-629-16

Query Match          9.0%; Score 19; DB 1; Length 190;
Best Local Similarity 100.0%; Pred. No. 7.1e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVSIRGVDGSLGLGMN 122
Db 71 AVGLVSIRGVDGSLGLGMN 89
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Db 101 AVGLVSIRGVDSGLYLGMN 119

RESULT 13

US-08-776-207-16
; Sequence 16, Application US/08776207A
; Patent No. 6080718
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Marc W.
; TITLE OF INVENTION: Receptor-Ligand Assay
; FILE REFERENCE: HU95-01A2
; CURRENT APPLICATION NUMBER: US/08/776,207A
; CURRENT FILING DATE: 1997-06-23
; EARLIER APPLICATION NUMBER: PCT/US95/09172
; EARLIER FILING DATE: 1995-07-19
; EARLIER APPLICATION NUMBER: 08/441,629
; EARLIER FILING DATE: 1995-05-15
; EARLIER APPLICATION NUMBER: 08/279,217
; EARLIER FILING DATE: 1994-07-22
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapien
US-08-776-207-16

Query Match 9.0%; Score 19; DB 3; Length 190;
Best Local Similarity 100.0%; Pred. No. 7.1e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVSIRGVDSGLYLGMN 122
Db 101 AVGLVSIRGVDSGLYLGMN 119

RESULT 14

PCT-US95-09172-16
; Sequence 16, Application PC/TUS9509172
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Marc W.
; APPLICANT: Kinoshita, Noriyuki
; TITLE OF INVENTION: RECEPTOR-LIGAND ASSAY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09172
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/279,217
; FILING DATE: 22-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/441,629
; FILING DATE: 15-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: HU95-01A PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240

; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 190 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-09172-16

Query Match 9.0%; Score 19; DB 5; Length 190;
Best Local Similarity 100.0%; Pred. No. 7.1e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVSIRGVDSGLYLGMN 122
Db 101 AVGLVSIRGVDSGLYLGMN 119

RESULT 15

US-08-438-439C-21
; Sequence 21, Application US/08438439C
; Patent No. 5876967
; GENERAL INFORMATION:
; APPLICANT: Nathans, Jeremy
; APPLICANT: Smallwood, Phillip M.
; APPLICANT: Macke, Jennifer P.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
; TITLE OF INVENTION: FACTOR-2 AND METHODS OF USE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,439C
; FILING DATE: May 12, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/046001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-438-439C-21

Query Match 9.0%; Score 19; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 7.2e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVSIRGVDSGLYLGMN 122
Db 101 AVGLVSIRGVDSGLYLGMN 119

Search completed: October 21, 2002, 16:21:17
Job time : 32 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: October 21, 2002, 16:17:56 ; Search time 20 Seconds
(without alignments)
1013.742 Million cell updates/sec

Title: US-09-817-814-2

Perfect score: 211

Sequence: 1 MAPLAEGGFLGGLGQQ.....PRPVDPERVELYKDLLMYT 211

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR_71.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	211	100.0	211	2	JC7353
2	85	40.3	212	2	JC7511
3	26	12.3	208	2	JC7082
4	19	9.0	208	2	S66486
5	19	9.0	208	2	A48137
6	16	7.6	207	2	JC5940
7	16	7.6	207	2	JC5941
8	8	3.8	151	2	E69134
9	8	3.8	157	2	G87417
10	8	3.8	197	2	A86430
11	8	3.8	226	2	T01363
12	8	3.8	545	2	T45935
13	8	3.8	564	2	F59092
14	8	3.8	756	2	T00367
15	8	3.8	1020	2	T42229
16	7	3.3	70	2	C83831
17	7	3.3	94	2	A64111
18	7	3.3	101	2	D82716
19	7	3.3	116	2	T37070
20	7	3.3	142	2	A29134
21	7	3.3	156	2	S41784
22	7	3.3	167	2	G95223
23	7	3.3	167	2	B98088
24	7	3.3	177	2	F82324
25	7	3.3	219	2	H71477
26	7	3.3	219	2	G81740
27	7	3.3	231	2	AB2538
28	7	3.3	236	2	A84644
29	7	3.3	238	2	T03968
30	7	3.3	242	1	S71250
31	7	3.3	246	1	A32999
32	7	3.3	251	2	F87242
33	7	3.3	255	2	S21498
34	7	3.3	262	2	T22599
35	7	3.3	262	2	T01305
36	7	3.3	262	2	H72590
37	7	3.3	274	2	G70500
38	7	3.3	278	2	E83336
39	7	3.3	314	2	S75685
40	7	3.3	316	2	T21044
41	7	3.3	316	2	T46505
42	7	3.3	330	2	G70792
43	7	3.3	388	2	C84051
44	7	3.3	391	1	RRNZYA
45	7	3.3	391	1	RRNZED
46	7	3.3	392	1	A70406
47	7	3.3	409	2	A48890
48	7	3.3	412	2	C38104
49	7	3.3	413	2	H88481
50	7	3.3	415	2	S37340
51	7	3.3	420	2	B38104
52	7	3.3	423	2	A72616
53	7	3.3	424	2	A38104
54	7	3.3	426	2	F81653
55	7	3.3	431	2	D71495
56	7	3.3	436	2	B82431
57	7	3.3	439	2	D72716
58	7	3.3	486	2	E87566
59	7	3.3	492	2	A33354
60	7	3.3	496	2	D97023
61	7	3.3	511	1	A48560
62	7	3.3	512	1	WMBEY4
63	7	3.3	589	2	T12820
64	7	3.3	627	1	JC6534
65	7	3.3	657	2	H71422
66	7	3.3	709	2	JH0126
67	7	3.3	709	2	AE3468
68	7	3.3	711	1	TFHUL
69	7	3.3	738	2	E85061
70	7	3.3	739	2	S06397
71	7	3.3	757	2	T42693
72	7	3.3	824	2	AD3098
73	7	3.3	829	2	F83499
74	7	3.3	829	2	D82430
75	7	3.3	834	2	E95346
76	7	3.3	834	2	E98188
77	7	3.3	863	2	T38016
78	7	3.3	875	2	F96027
79	7	3.3	1012	2	T13603
80	7	3.3	1025	2	S69790
81	7	3.3	1058	2	B95292
82	7	3.3	1128	1	QBE47
83	7	3.3	1418	2	D75281
84	7	3.3	1536	2	S59841
85	7	3.3	1607	2	T02837
86	7	3.3	2163	2	T15276
87	7	3.3	3390	1	GNWVD3
88	7	3.3	4302	2	A38971
89	7	3.3	13055	2	T16580
90	6	2.8	27	2	S29211
91	6	2.8	31	2	S03775
92	6	2.8	47	2	S78335
93	6	2.8	56	1	CBBOC6
94	6	2.8	57	2	S07344
95	6	2.8	61	2	G95882
96	6	2.8	64	2	B82672
97	6	2.8	66	2	S61083
98	6	2.8	68	2	I40461
99	6	2.8	78	2	S69531
100	6	2.8	86	2	JH0445
101	6	2.8	86	2	A96968
102	6	2.8	90	2	C84841

glutathione peroxi
myelin P0 protein
probable secreted
bclA protein - Rho
1-acylglycerol-3-p
hypothetical prote
hypothetical prote
hypothetical prote
cytochrome c bioge
hypothetical prote
hypothetical prote
hypothetical prote
multidrug resistan
polymerase-associa
transporter (major
transcription acti
LFY floral meriste
protein let-756 (i
LFY floral meriste
probable glutamate
LFY floral meriste
tollB protein, prob
probable polysacch
regulatory protein
hypothetical prote
hypothetical prote
UL 41 protein - hu
threonine synthase
UL54 protein - hum
hypothetical prote
protein kinase 1 (i
hypothetical prote
moBA protein precu
diacylate cyclas
lactotransferrin p
probable homeotic
photosystem I prot
hypothetical prote
periplasmic nitrat
periplasmic nitrat
NAPa periplasmic n
periplasmic nitrat
importin beta-1 su
probable malcoolig
probable N-methyl-
fibronectin-bindin
probable adenylate
DNA-binding protei
ribonucleoside-dip
4-alpha-glucanotra
long chain fatty a
hypothetical prote
genome polyprotein
polycystic kidney
hypothetical prote
probable phospholi
hypothetical prote
hypothetical prote
cytochrome b-c1 co
nef protein - huma
hypothetical prote
hypothetical prote
M protein precurs
mersacidin precurs
holin protein - ph
hypothetical 10.2K
hypothetical prote
hypothetical prote

103	6	2.8	91	2	G75015	acylphosphatase (a	176	2.8	178	2	S00528	vega protein - myc
104	6	2.8	95	2	T17894	hypothetical prote	177	2.8	180	2	D83636	conserved hypothet
105	6	2.8	99	2	B84841	hypothetical prote	178	2.8	182	2	S03247	nef protein (clone
106	6	2.8	100	2	D72708	hypothetical prote	179	6	183	2	E82212	hypothetical prote
107	6	2.8	101	2	AG3458	urease beta chain	180	6	184	2	C83373	hypothetical prote
108	6	2.8	101	2	C90239	acylphosphatase [1	181	6	184	2	H75329	conserved hypothet
109	6	2.8	106	2	D97815	hypothetical prote	182	6	185	2	T36874	hypothetical prote
110	6	2.8	107	1	B36950	urease (EC 3.5.1.5	183	6	187	2	S23585	embryonic fibrobla
111	6	2.8	107	2	H84658	hypothetical prote	184	6	188	1	F64494	conserved hypothet
112	6	2.8	108	2	AE2264	urease beta chain	185	6	189	2	H70042	transcription regu
113	6	2.8	108	2	SA0292	protein-tyrosine-p	186	6	191	2	B84272	protoporphyrinogen
114	6	2.8	111	2	G34768	hypothetical prote	187	6	191	2	AG3068	conserved hypothet
115	6	2.8	112	2	A13297	hypothetical prote	188	6	191	2	D98218	hypothetical prote
116	6	2.8	114	2	T33802	hypothetical prote	189	6	191	2	G90966	hypothetical prote
117	6	2.8	115	2	S22738	hypothetical prote	190	6	191	2	G85814	probable outer mem
118	6	2.8	117	2	A89964	hypothetical prote	191	6	192	2	S54407	embryonic fibrobla
119	6	2.8	118	1	B70021	arsenate reductase	192	6	193	2	H91249	hypothetical prote
120	6	2.8	118	2	T03756	hypothetical prote	193	6	194	2	S25106	fibroblast growth
121	6	2.8	121	1	S10031	urease (EC 3.5.1.5	194	6	198	2	S48749	cytochrome p460 pr
122	6	2.8	121	2	H25007	hypothetical prote	195	6	198	2	F98312	hypothetical prote
123	6	2.8	121	2	C68145	urease (beta subun	196	6	200	2	AD3207	transcription regu
124	6	2.8	124	2	C69729	urease beta subuni	197	6	201	2	AE1880	transposase alr059
125	6	2.8	124	2	E83681	urease complex com	198	6	202	1	TVMSHS	fibroblast growth
126	6	2.8	124	2	H82890	beta-galactoside-b	199	6	204	2	S24985	nef protein - huma
127	6	2.8	129	2	D28302	hypothetical prote	200	6	205	1	ASLJH3	nef protein - huma
128	6	2.8	131	2	G72628	hypothetical prote	201	6	205	1	ASLJTK	nef protein - huma
129	6	2.8	133	2	D70911	hypothetical prote	202	6	205	2	S43467	nef protein - huma
130	6	2.8	134	2	B84961	outer membrane por	203	6	205	2	T35505	hypothetical prote
131	6	2.8	135	2	B69103	translation initia	204	6	206	1	TVHUIS	fibroblast growth
132	6	2.8	136	2	D90027	urease beta subuni	205	6	206	1	ASLJ12	nef protein - huma
133	6	2.8	141	2	S52446	Ig heavy chain V r	206	6	206	1	ASLJLV	nef protein - huma
134	6	2.8	141	2	T33836	hemoglobin - sludg	207	6	206	1	ASLJFV	nef protein - huma
135	6	2.8	142	2	T42849	hypothetical prote	208	6	206	2	JC4268	fibroblast growth
136	6	2.8	143	1	WZBE32	gene 32 protein -	209	6	206	2	S03244	nef protein (clone
137	6	2.8	143	1	E70980	hypothetical prote	210	6	206	2	S03245	nef protein (clone
138	6	2.8	143	2	G71980	hypothetical prote	211	6	206	2	S35937	nef protein - huma
139	6	2.8	144	2	AB0325	urease (EC 3.5.1.5	212	6	206	2	S35986	nef protein - huma
140	6	2.8	144	2	H71853	hypothetical prote	213	6	207	1	QQLJND	hypothetical prote

249	6	2.8	231	2	AF3028	hypothetical prote	322	6	2.8	281	2	C87073	conserved hypothet
250	6	2.8	231	2	C81981	probable sugar-pho	333	6	2.8	282	2	AG3112	hypothetical prote
251	6	2.8	231	2	S50462	hypothetical prote	334	6	2.8	282	2	D81089	RplR/YebK/YfhH fam.
252	6	2.8	232	2	S42392	G-box-binding prot	335	6	2.8	283	2	T26397	hypothetical prote
253	6	2.8	234	2	S61309	nitrate reductase	336	6	2.8	283	2	S52928	XSGU1 protein - Af
254	6	2.8	235	2	T31424	C-terminal domain-	337	6	2.8	283	2	S39602	class I histocompa
255	6	2.8	236	2	S51332	ubiquitin thiolest	338	6	2.8	283	2	S42393	G-box-binding prot
256	6	2.8	236	2	B40609	probable lipoprote	339	6	2.8	284	2	T23158	hypothetical prote
257	6	2.8	236	2	A53853	apolipoprotein B m	339	6	2.8	284	2	F98174	oligopeptide ABC t
258	6	2.8	237	1	S33290	25K outer-membrane	331	6	2.8	284	2	E70232	hypothetical prote
259	6	2.8	238	2	T46166	urease (EC 3.5.1.5	332	6	2.8	284	2	T28887	collagen dpv-10 -
260	6	2.8	238	2	S49911	MYB27 protein - Ar	333	6	2.8	284	2	S74256	homeotic protein s
261	6	2.8	239	2	S37923	hypothetical prote	334	6	2.8	285	2	S72787	hypothetical prote
262	6	2.8	239	2	H75293	cell wall protein	335	6	2.8	285	2	A75629	hypothetical prote
263	6	2.8	241	2	AH3628	probable manganese	336	6	2.8	285	2	C83254	probable hydrolase
264	6	2.8	242	1	BVECR0	respiratory nitrat	337	6	2.8	288	2	T17664	probable aspartate
265	6	2.8	242	2	G91057	DNA repair protein	338	6	2.8	288	2	G64425	branched-chain ami
266	6	2.8	242	2	D85902	DNA repair protein	339	6	2.8	288	2	AI0810	pyridoxal kinase (
267	6	2.8	242	2	AI0828	DNA repair protein	340	6	2.8	291	2	G70605	probable hydrolase
268	6	2.8	242	2	C71006	hypothetical prote	341	6	2.8	291	2	AE0298	conserved hypothet
269	6	2.8	243	2	A86832	conserved hypothet	342	6	2.8	292	2	D83580	probable transcrip
270	6	2.8	243	2	S44914	ZK688.7 protein -	343	6	2.8	293	2	P90978	hypothetical prote
271	6	2.8	244	2	A41021	NAD+--asparagine A	344	6	2.8	293	2	E86474	unknown protein li
272	6	2.8	244	2	T41676	hypothetical prote	345	6	2.8	294	2	T10690	serine/threonine-s
273	6	2.8	246	1	NDPS7A	type II site-speci	346	6	2.8	294	2	S59774	probable membrane
274	6	2.8	246	2	S58497	early auxin-induci	347	6	2.8	294	2	A90542	hypothetical prote
275	6	2.8	246	2	AB0319	probable glutamate	348	6	2.8	295	2	S67919	transcription regu
276	6	2.8	248	2	B90890	hypothetical prote	349	6	2.8	296	2	A64035	hypothetical prote
277	6	2.8	251	1	G71366	hypothetical prote	350	6	2.8	296	2	G84337	methionyl aminopep
278	6	2.8	251	1	JC4750	probable uridylyate	351	6	2.8	296	2	G90063	hypothetical prote
279	6	2.8	251	1	ASLJSZ	qEg16 protein -	352	6	2.8	297	2	S01176	hypothetical prote
280	6	2.8	255	1	ASLJCZ	nef protein - huma	353	6	2.8	298	2	T29297	hypothetical prote
281	6	2.8	255	2	T44040	uracil-DNA glycosy	354	6	2.8	300	1	A32566	ubiquinol--cytochr
282	6	2.8	255	2	T44226	uracil-DNA glycosy	355	6	2.8	300	2	G89915	conserved hypothet
283	6	2.8	255	2	T28121	hypothetical prote	356	6	2.8	301	2	T35805	hypothetical prote
284	6	2.8	257	2	T03136	hypothetical prote	357	6	2.8	302	2	AB0510	citg protein limpo
285	6	2.8	257	2	C84890	hypothetical prote	358	6	2.8	302	2	F75619	probable hemin ABC
286	6	2.8	257	2	AB4390	thiosulfate sulfur	359	6	2.8	304	2	B75486	probable snog prot
287	6	2.8	260	1	ASLJCZ	nef protein - huma	360	6	2.8	304	2	S59965	phosphotransferase
288	6	2.8	261	2	J01024	hypothetical 30K P	361	6	2.8	304	2	F84298	hypothetical prote
289	6	2.8	261	2	B95273	hypothetical prote	362	6	2.8	306	2	G86593	Yop translocation
290	6	2.8	262	2	T31305	4-hydroxy-2-oxoval	363	6	2.8	306	2	C71498	probable yop trans
291	6	2.8	262	2	E90865	probable transient	364	6	2.8	306	2	C72030	type III secretion
292	6	2.8	262	2	D85753	probable transient	365	6	2.8	306	2	F97600	hypothetical prote
293	6	2.8	263	2	A75280	phenylacetic acid	366	6	2.8	307	1	S18524	fructokinase (EC 2
294	6	2.8	264	2	A36207	fibroblast growth	367	6	2.8	307	2	AH3374	transporter, dme f
295	6	2.8	264	2	AB2295	conserved hypothet	368	6	2.8	309	2	JC4958	serine hydroxymeth
296	6	2.8	264	2	AB1429	an E. coli protein	369	6	2.8	309	2	T31135	hypothetical prote
297	6	2.8	265	2	AI1802	probable lipote-p	370	6	2.8	310	2	S15096	collagen alpha 1(I
298	6	2.8	265	2	T35309	hypothetical prote	371	6	2.8	310	2	G83248	probable permease
299	6	2.8	265	2	E64880	fibroblast growth	372	6	2.8	310	2	T50879	phytoene synthase
300	6	2.8	266	2	S68144	nitrate transport	373	6	2.8	312	2	B37245	1-phosphofructokin
301	6	2.8	266	2	AE3609	fibroblast growth	374	6	2.8	312	2	D91011	fructose-1-phospha
302	6	2.8	267	1	TVHUF5	fibroblast growth	375	6	2.8	312	2	F85855	fructose-1-phospha
303	6	2.8	267	2	C83979	myo-inositol-1(or	376	6	2.8	312	2	AF0158	1-phosphofructokin
304	6	2.8	267	2	G83206	hypothetical prote	377	6	2.8	312	2	AE0783	1-phosphofructokin
305	6	2.8	267	2	G84319	orotidine-5'-monop	378	6	2.8	313	1	BESMHP	mannosyl-glycoprot
306	6	2.8	270	2	B84813	probable RING zinc	379	6	2.8	313	2	AG4069	1-phosphofructokin
307	6	2.8	272	2	H70335	hypothetical prote	380	6	2.8	315	2	AG2012	hypothetical prote
308	6	2.8	272	2	T49898	CCAAT box binding	381	6	2.8	316	1	FWYCG	H+-transporting tw
309	6	2.8	273	2	H70015	hypothetical prote	382	6	2.8	317	2	I37371	ER calcium-binding
310	6	2.8	273	2	G69770	manganese-containi	383	6	2.8	318	2	T44792	2-keto-3-deoxygluc
311	6	2.8	274	2	E83423	conserved hypothet	384	6	2.8	318	2	E96033	probable sugar upt
312	6	2.8	275	2	T36573	probable partition	385	6	2.8	318	2	D83330	transcription regu
313	6	2.8	276	2	S35270	DNA-damage repair	386	6	2.8	320	2	A75278	probable cobW prot
314	6	2.8	277	1	D35115	indole-3-glycerol-	387	6	2.8	322	2	AH0903	octaprenyl-diphosp
315	6	2.8	278	2	AD3253	chromosome partiti	388	6	2.8	323	2	S16318	homeotic protein H
316	6	2.8	278	2	E87704	hypothetical prote	389	6	2.8	324	2	E83320	conserved hypothet
317	6	2.8	279	2	F71123	probable sugar tra	390	6	2.8	326	2	B69412	transcription init
318	6	2.8	279	2	D97024	hypothetical prote	391	6	2.8	326	2	B87557	hypothetical prote
319	6	2.8	280	2	S72844	beta-aspartate met	392	6	2.8	326	2	S27534	hypothetical prote
320	6	2.8	280	2	A70513	hypothetical prote	393	6	2.8	327	2	G85727	probable transport
321	6	2.8	281	2	A72472	probable electron	394	6	2.8	328	2	B87697	conserved hypothet

395	6	2.8	328	2	G97017	uncharacterized me	468	2.8	376	2	E70918	hypothetical prote
396	6	2.8	329	2	C97264	UDP-galactose 4-ep	469	2.8	376	2	T39454	hypothetical prote
397	6	2.8	329	2	F95298	aldehyde or keto o	470	2.8	376	2	A96951	TPR-repeat-contain
398	6	2.8	330	2	S74255	homeotic protein s	471	2.8	377	2	S76013	heat shock protein
399	6	2.8	331	2	S50212	bis(9'nucleo) tetr	472	2.8	377	2	G85975	hypothetical prote
400	6	2.8	331	2	A36358	T-cell acute lymph	473	2.8	378	2	S04336	u1 snRNP 70K prote
401	6	2.8	332	2	H83069	probable c4'-dicarb	474	2.8	378	2	C85431	hypothetical prote
402	6	2.8	333	2	B84195	hypothetical prote	475	2.8	379	2	T50751	hydroxyneurosporen
403	6	2.8	333	2	T29242	hypothetical prote	476	2.8	379	2	D70786	probable gcvt prot
404	6	2.8	335	2	B72668	hypothetical prote	477	2.8	379	2	C84577	probable nucleosom
405	6	2.8	337	2	A83216	ABC transporter, m	478	2.8	381	2	G64612	rod shape-determin
406	6	2.8	339	2	T11751	transcription repr	479	2.8	381	2	A64783	ybbZ protein - Esc
407	6	2.8	339	2	C96508	hypothetical prote	480	2.8	381	2	H90700	glycerate kinase I
408	6	2.8	340	2	A64902	peptide transport	481	2.8	381	2	C85551	glycerate kinase I
409	6	2.8	340	2	A10392	thiamin biosynthes	482	2.8	382	2	E70719	probable fadE13 pr
410	6	2.8	341	2	A60675	probable alcohol d	483	2.8	383	2	B69232	conserved hypotet
411	6	2.8	341	2	T34693	hypothetical prote	484	2.8	383	2	T26902	hypothetical prote
412	6	2.8	341	2	E83340	hypothetical prote	485	2.8	383	2	AH3457	acriflavin resista
413	6	2.8	342	2	D75184	probable RNA-3'-ph	486	2.8	384	2	G91130	N-acetylglucosam
414	6	2.8	342	2	T22428	hypothetical prote	487	2.8	384	2	G82976	probable rubredoxi
415	6	2.8	343	1	D33858	mercury(II) reduct	488	2.8	385	2	S28360	Al1 protein - beet
416	6	2.8	344	2	H72213	N utilization subs	489	2.8	387	2	A82014	capsule polysaccha
417	6	2.8	346	1	S35500	heterogeneous ribo	490	2.8	388	2	B89925	chorismate synthas
418	6	2.8	346	2	A45885	MHC class I histoc	491	2.8	389	2	T08128	probable sedoheptu
419	6	2.8	347	2	E95194	D-alanine-D-alani	492	2.8	389	2	T08135	sedoheptulose-bisp
420	6	2.8	347	2	B98061	D-alanine-D-alani	493	2.8	390	1	RRBPT4	recombination/rep
421	6	2.8	348	2	B75312	branched-chain ami	494	2.8	390	2	H87345	thiolase family pr
422	6	2.8	349	2	J02300	replicase - pepper	495	2.8	391	2	G82320	probable oxygen-in
423	6	2.8	349	2	S31875	Al1 protein - pepp	496	2.8	391	2	S15220	capsule polysaccha
424	6	2.8	349	2	E89795	conserved hypotet	497	2.8	391	2	AD2501	hypothetical prote
425	6	2.8	351	2	J02327	Al1 protein - Indi	498	2.8	391	2	H98138	hypothetical prote
426	6	2.8	352	1	QCCLV1	Al1 protein - toma	499	2.8	391	2	AC3149	glycosyltransferas
427	6	2.8	355	1	QOCVW1	AV1 protein - abut	500	2.8	392	2	H83198	probable MFS trans
428	6	2.8	355	2	E83741	hypothetical prote	501	2.8	393	2	T03216	enoyl-lacyl-carrie
429	6	2.8	356	2	F84072	hypothetical prote	502	2.8	393	2	E97761	hypothetical prote
430	6	2.8	357	1	QOCVC1	Al1 protein - toma	503	2.8	394	2	B75404	probable amidase -
431	6	2.8	358	1	J01870	Al1 protein - toma	504	2.8	394	2	T37520	arginase family pr
432	6	2.8	358	2	S44233	strP protein - Str	505	2.8	395	2	H75457	hypothetical prote
433	6	2.8	358	2	I38920	prostaglandin E2 r	506	2.8	397	2	AG0490	probable Arac-fam1
434	6	2.8	358	2	S13132	EP2 prostaglandin	507	2.8	398	2	I56540	protein-tyrosine-p
435	6	2.8	358	2	S07594	hypothetical prote	508	2.8	398	2	G90225	hypothetical prote
436	6	2.8	359	2	S22593	hypothetical prote	509	2.8	398	2	A58922	esterase/N-deacety
437	6	2.8	359	2	S39211	gene C1 protein -	510	2.8	398	2	AE3577	sugar-binding prot
438	6	2.8	359	2	S39235	gene C1 protein -	511	2.8	399	2	A83354	hypothetical prote
439	6	2.8	359	2	T39944	hypothetical trans	512	2.8	401	1	QXBP1L	hypothetical prote
440	6	2.8	360	2	B36470	Wnt-2 protein - mo	513	2.8	401	2	T51493	stearoyl-acyl carr
441	6	2.8	360	2	S00834	int-1-like protein	514	2.8	401	2	T19771	hypothetical prote
442	6	2.8	360	2	AE0172	probable outer mem	515	2.8	402	2	T52356	related to GTP-bin
443	6	2.8	360	2	S59885	replication-associ	516	2.8	403	2	E71300	probable protein-g
444	6	2.8	360	2	H87699	conserved hypotet	517	2.8	404	2	AF3236	thermophilic desul
445	6	2.8	361	1	QOCVPT	Al1 protein - pota	518	2.8	405	2	D81918	sodium-translocati
446	6	2.8	361	2	S32168	dimethylallyltrans	519	2.8	405	2	G81184	Na(+)-translocati
447	6	2.8	362	1	J01887	Al1 protein - toma	520	2.8	406	2	C75537	conserved hypotet
448	6	2.8	362	2	A71243	probable maltose/m	521	2.8	407	1	S65531	sodium-translocati
449	6	2.8	362	2	A75208	sugar transport AT	522	2.8	407	2	E71665	bicyclomycin resis
450	6	2.8	365	1	MMBP2	outer membrane por	523	2.8	407	2	E98347	hypothetical prote
451	6	2.8	365	1	MMPCNC	outer membrane por	524	2.8	407	2	AB2935	conserved hypotet
452	6	2.8	365	2	A83727	naringenin-chalcon	525	2.8	408	2	B82094	sodium-translocati
453	6	2.8	366	2	A86837	conserved hypotet	526	2.8	409	2	AG2869	N-carbamoyl-beta-a
454	6	2.8	366	2	AH2429	hypothetical prote	527	2.8	411	1	D64052	Na+-translocating
455	6	2.8	367	2	T44888	probable aminometh	528	2.8	413	2	E84120	serine hydroxymeth
456	6	2.8	367	2	T48692	hypothetical prote	529	2.8	413	2	H83833	hypothetical prote
457	6	2.8	368	2	C69590	chorismate synthas	530	2.8	414	1	H69963	DNA-damage repair
458	6	2.8	369	2	S60063	succinyl-diaminopi	531	2.8	415	2	A97646	n-carbamoyl-beta-a
459	6	2.8	369	2	J01974	HTF9-C protein - m	532	2.8	415	2	T00678	hypothetical prote
460	6	2.8	369	2	A75166	hypothetical prote	533	2.8	417	2	E75303	aminopeptidase - D
461	6	2.8	370	2	E71221	hypothetical prote	534	2.8	418	2	E71848	probable nucleosid
462	6	2.8	371	2	S76682	hypothetical prote	535	2.8	418	2	D64667	pyrimidine nucleos
463	6	2.8	372	2	A42778	agglutinin precurs	536	2.8	418	2	S77640	exopolysaccharide
464	6	2.8	373	2	AB1224	cobalamin biosynth	537	2.8	419	2	G71311	probable phosphogl
465	6	2.8	373	2	H84404	ferrichrome ABC tr	538	2.8	419	2	G70652	probable sers prot
466	6	2.8	373	1	G07036	IMP dehydrogenase	539	2.8	419	2	H95357	probable TtuD3 hyd
467	6	2.8	375	2	H83290	conserved hypotet	540	2.8	419	2	G90264	hypothetical prote

541	6	2.8	422	2	D72302	hypotheical prote	614	6	2.8	469	2	A24450	collagen alpha 2(V
542	6	2.8	425	2	E83023	3-deoxy-D-manno-oc	615	6	2.8	469	2	B87094	yadQ protein - Esc
543	6	2.8	426	2	C70896	glycine hydroxymet	616	6	2.8	473	2	C64739	probable channel t
544	6	2.8	426	2	D87153	serine hydroxymeth	617	6	2.8	473	2	G90648	probable channel t
545	6	2.8	426	2	F83420	ATP-dependent Clp	618	6	2.8	473	2	G85499	hypotheical prote
546	6	2.8	427	2	C84966	3-phosphoshikimate	619	6	2.8	474	2	T19543	hypotheical prote
547	6	2.8	427	2	E72488	probable tryptopha	620	6	2.8	475	2	T45766	probable Zn-depend
548	6	2.8	427	2	AD2603	components of type	621	6	2.8	475	2	G96927	retinoic acid rece
549	6	2.8	428	2	E84192	zinc metalloprotei	622	6	2.8	476	2	B41977	transcription fact
550	6	2.8	428	2	F87038	probable membrane	623	6	2.8	480	2	A40815	hypotheical prote
551	6	2.8	429	2	A56265	uracil transport p	624	6	2.8	481	2	S56299	hypotheical prote
552	6	2.8	429	2	G91048	uracil transport E	625	6	2.8	482	2	E96985	altronate oxidore
553	6	2.8	429	2	C85893	uracil transport p	626	6	2.8	482	2	S76475	hypotheical prote
554	6	2.8	429	2	AG0818	uracil permease (u	627	6	2.8	483	2	H87492	yJef family protei
555	6	2.8	429	2	C87580	Xaa-Pro dipeptidas	628	6	2.8	483	2	T36811	probable integral
556	6	2.8	431	2	T07685	omega-3 fatty acid	629	6	2.8	483	2	AC0913	sodium/pantothenat
557	6	2.8	431	2	G83404	probable chemotaxi	630	6	2.8	484	1	A46217	GPI-anchor biosynt
558	6	2.8	431	2	J50055	hypotheical 43.7K	631	6	2.8	484	2	A86503	pyruvate kinase [l
559	6	2.8	432	2	S38893	uracil transport p	632	6	2.8	484	2	A72119	pyruvate kinase CP
560	6	2.8	432	2	T24072	hypotheical prote	633	6	2.8	484	2	H64105	pantothenate trans
561	6	2.8	433	2	H70141	enolase (eno) homo	634	6	2.8	484	2	AB0445	sodium/pantothenat
562	6	2.8	433	2	A70536	probable pepC prot	635	6	2.8	485	1	A55731	GPI-anchor biosynt
563	6	2.8	434	2	A57986	membrane-bound ura	636	6	2.8	485	2	I52484	gene FIG-A protein
564	6	2.8	434	2	F90184	cobyrinic acid A,C	637	6	2.8	485	2	D65118	pantothenate perme
565	6	2.8	435	2	E86266	protein F3F19.23 [638	6	2.8	485	2	B91145	sodium/pantothenat
566	6	2.8	436	2	F82422	anaerobic glycerol	639	6	2.8	485	2	F85990	sodium/pantothenat
567	6	2.8	438	2	H71674	proline/betaine tr	640	6	2.8	486	2	S76523	serine-type D-Ala-
568	6	2.8	438	2	A72430	hypotheical prote	641	6	2.8	486	2	D70439	conserved hypotet
569	6	2.8	438	2	S35787	collagen alpha cha	642	6	2.8	489	2	H86711	4-alpha-glucanotr
570	6	2.8	438	2	F81659	D-alanyl-D-alanine	643	6	2.8	490	2	B86265	cytochrome P450 7I
571	6	2.8	439	2	D83345	L-sorbose dehydr	644	6	2.8	491	2	S48827	1-aminocyclopropan
572	6	2.8	440	2	I50213	protein-tyrosine-p	645	6	2.8	492	2	S61242	virion serine/thre
573	6	2.8	440	2	C84832	probable methionyl	646	6	2.8	495	2	T13019	1-aminocyclopropan
574	6	2.8	440	2	C82410	conserved hypotet	647	6	2.8	495	2	G95147	polysaccharide bio
575	6	2.8	441	2	C87233	probable cell inva	648	6	2.8	495	2	T05388	hypotheical prote
576	6	2.8	441	2	E90051	hypotheical prote	649	6	2.8	495	2	E98015	conserved hypotet
577	6	2.8	442	2	A83122	probable MFS trans	650	6	2.8	496	2	AI0907	probable sialic ac
578	6	2.8	442	2	G86294	T24D18.11 protein	651	6	2.8	498	2	C83717	NADP-dependent ald
579	6	2.8	442	2	A12272	hypotheical prote	652	6	2.8	500	2	A41552	aldosterone syntha
580	6	2.8	443	2	H87185	aminopeptidase I [653	6	2.8	500	2	E87009	probable two-compo
581	6	2.8	444	2	T20374	hypotheical prote	654	6	2.8	501	2	A38650	myosin heavy chain
582	6	2.8	445	2	T49556	epithelial zinc-fi	655	6	2.8	501	2	T36051	probable cytochrom
583	6	2.8	446	2	T17018	1-aminocyclopropan	656	6	2.8	501	2	E70596	hypotheical prote
584	6	2.8	446	2	C81058	hypotheical prote	657	6	2.8	503	2	T38997	vacuolar atp synth
585	6	2.8	446	2	A83355	hypotheical prote	658	6	2.8	503	2	S25335	H+-transporting AT
586	6	2.8	446	2	H85076	probable athila tr	659	6	2.8	503	2	D70926	hypotheical prote
587	6	2.8	447	2	F82619	proton glutamate s	660	6	2.8	503	2	D98116	hypotheical prote
588	6	2.8	449	2	I39489	L-sorbose dehydr	661	6	2.8	503	2	G95251	conserved hypotet
589	6	2.8	450	2	G01158	tyrosine kinase ac	662	6	2.8	504	2	JC1306	virion protein hom
590	6	2.8	451	2	D84091	hypotheical' prote	663	6	2.8	504	2	G02474	interferon regulat
591	6	2.8	452	2	B90407	conserved hypotet	664	6	2.8	504	2	H87672	conserved hypotet
592	6	2.8	452	2	H75379	conserved hypotet	665	6	2.8	505	2	T46996	hypotheical prote
593	6	2.8	454	2	D70904	probable mcal prot	666	6	2.8	505	2	AG0239	succinylglutamic s
594	6	2.8	456	2	T06589	3-methyl-2-oxobuta	667	6	2.8	505	2	G70954	probable lysS prot
595	6	2.8	456	2	T40367	n-acetylglucosamin	668	6	2.8	505	2	C53153	glucose transport
596	6	2.8	456	2	T39014	hypotheical zinc-	669	6	2.8	505	2	AC3361	GTP-binding protei
597	6	2.8	457	2	S03961	Ig mu chain C regi	670	6	2.8	506	2	B65114	probable sialic ac
598	6	2.8	459	2	A75097	hypotheical prote	671	6	2.8	506	2	A91141	sialic acid transp
599	6	2.8	459	2	T21167	hypotheical prote	672	6	2.8	506	2	D85986	sialic acid transp
600	6	2.8	460	2	H87396	conserved hypotet	673	6	2.8	506	2	S65193	hypotheical prote
601	6	2.8	461	2	A31237	alpha-2C-adrenergi	674	6	2.8	508	1	PKMWA	H+-transporting tw
602	6	2.8	462	1	A41326	enantiomer-selecti	675	6	2.8	508	2	T22440	hypotheical prote
603	6	2.8	462	2	D32057	nitrogenase (EC 1.	676	6	2.8	510	2	A55207	glycerol-3-phospha
604	6	2.8	462	2	D97385	cpaE protein (AF22	677	6	2.8	510	2	AH0366	probable sugar tra
605	6	2.8	463	2	C70931	probable PPE prote	678	6	2.8	510	2	H87320	conserved hypotet
606	6	2.8	464	2	B81817	probable integral	679	6	2.8	512	2	B83197	glycerol-3-phospha
607	6	2.8	464	2	B55223	major tail protein	680	6	2.8	512	2	A54400	protein kinase (EC
608	6	2.8	465	1	WMBE28	UL38 protein - hum	681	6	2.8	513	2	A99839	Na+/H+ antiporter
609	6	2.8	465	1	WMBE44	maturatation protei	682	6	2.8	513	2	G64864	Na+/H+ exchanging
610	6	2.8	465	2	G95973	endo-1,3-1,4-beta-	683	6	2.8	513	2	A85697	Na+/H+ antiporter,
611	6	2.8	466	1	WMBEHT	capsid protein ICP	684	6	2.8	513	2	AD3505	7.5K chlorosome pr
612	6	2.8	466	2	A95355	probable inner-mem	685	6	2.8	514	2	AG0723	regulator of intra
613	6	2.8	467	2	T10879	y41C protein - Rhi	686	6	2.8	515	2	A70905	hypotheical prote

587	6	2.8	516	1	JC1172	histidine ammonia-	760	619	2	AI3336	potassium/proton a
588	6	2.8	516	2	JE0301	inulinase (EC 3.2.	761	620	2	S48772	AFRI protein - yea
589	6	2.8	516	2	H71332	hypothetical prote	762	621	2	S10450	myosin heavy chain
590	6	2.8	519	2	T07026	ethylene receptor	763	625	2	D83753	PTS system, fructo
591	6	2.8	520	2	C87450	GMP synthase [impo	764	625	2	D86244	protein Ser/Thr pr
592	6	2.8	523	2	T20828	hypothetical prote	765	627	2	T47968	dynamin-like prote
593	6	2.8	527	2	AD1346	propionate CoA-tra	766	628	2	T08942	proton pump intera
594	6	2.8	527	2	AG1716	propionate CoA-tra	767	628	2	G84481	probable receptor-
595	6	2.8	528	2	JC4814	Na+/H+-exchanging	768	629	2	T34726	probable dehydroge
596	6	2.8	530	2	G70904	hypothetical prote	769	632	2	B83163	probable AMP-bindi
597	6	2.8	530	2	C82144	Na+/H+ antiporter	770	634	2	T36614	hypothetical prote
598	6	2.8	531	2	D70946	NADH dehydrogenase	771	635	2	H69626	PTS fructose-speci
599	6	2.8	531	2	T35226	nitrate reductase	772	635	2	T07794	ethylene receptor
700	6	2.8	532	2	D69281	CTP synthase (pyrG	773	636	2	S41067	collagen alpha 1(I
701	6	2.8	535	1	A33813	sterol 26-monooxyg	774	637	2	B81939	probable threonine
702	6	2.8	535	2	C95057	CTP synthase [impo	775	637	2	E81167	threonyl-tRNA synt
703	6	2.8	535	2	F97926	CTP synthase (EC 6	776	644	2	JC5119	anti-mullerian hor
704	6	2.8	535	2	S74703	hypothetical prote	777	645	2	A75533	probenazole
705	6	2.8	537	2	T28683	hypothetical prote	778	646	2	A85834	hypothetical prote
706	6	2.8	538	2	F83622	probable permease	779	648	2	T45575	probable chaperoni
707	6	2.8	539	2	D96562	unknown protein [i	780	650	2	T21498	hypothetical prote
708	6	2.8	540	2	E71503	probable adp/atp t	781	651	2	B96665	hypothetical prote
709	6	2.8	545	2	B70374	conserved hypothet	782	652	2	A37000	leukemia virus rec
710	6	2.8	545	2	G90420	threonyl-tRNA synt	783	652	2	I48083	amphotropic murine
711	6	2.8	547	2	C96667	probable galactose	784	653	2	D69815	conserved hypothet
712	6	2.8	555	2	S22634	unknown protein, 7	785	654	2	A96235	hydroxamate-depend
713	6	2.8	556	2	B28182	sphingomyelin phos	786	654	2	AC3051	hypothetical prote
714	6	2.8	557	2	B82984	hemolysin B - Serr	787	655	2	T15879	hypothetical prote
715	6	2.8	558	2	B82984	hypothetical prote	788	655	2	S54183	acyl-CoA dehydroge
716	6	2.8	559	2	AH1719	pheromone ABC tran	789	656	2	S73313	hypothetical prote
717	6	2.8	562	2	S44664	probable membrane	790	656	2	A49579	amphotropic murine
718	6	2.8	563	2	AC2923	conserved hypothet	791	660	2	B70662	probable membranep
719	6	2.8	563	2	G97697	hypothetical prote	792	660	2	E98169	serine proteinase
720	6	2.8	564	2	E98291	probable 3,4-dihyd	793	660	2	AB3118	hypothetical prote
721	6	2.8	564	2	AE2992	3,4-dihydroxy-2-bu	794	662	2	T20570	interferon-induced
722	6	2.8	564	2	H86278	F14L17.20 protein	795	662	2	A33481	IL12 receptor comp
723	6	2.8	569	2	S47277	gp88 protein - mur	796	662	2	I37892	hypothetical prote
724	6	2.8	570	2	C98985	DNA-dependent RNA	797	662	2	S56781	betr protein homol
725	6	2.8	572	2	F90297	ATP-dependent RNA	798	666	2	D64137	hypothetical prote
726	6	2.8	576	1	NDBSR1	type II site-speci	799	669	2	T10666	hypothetical prote
727	6	2.8	576	2	C87261	hypothetical prote	800	670	2	S52673	probable membrane
728	6	2.8	576	2	T18067	hypothetical prote	801	672	2	F81990	NADH dehydrogenase
729	6	2.8	577	2	T40297	membrane transport	802	674	2	D81220	NADH dehydrogenase
730	6	2.8	580	2	T45022	transducer-like pr	803	674	2	T15524	hypothetical prote
731	6	2.8	581	1	F70423	DNA polymerase bet	804	674	2	S61181	hypothetical prote
732	6	2.8	582	2	A57068	protein-tyrosine-p	805	680	2	T45736	hypothetical prote
733	6	2.8	586	2	T52148	transport protein	806	682	2	T36877	probable regulator
734	6	2.8	589	1	R8APBQ	RNA-directed RNA p	807	682	2	T18847	hypothetical prote
735	6	2.8	589	2	T05074	hypothetical prote	808	690	2	D75487	v-type ATP synthas
736	6	2.8	589	2	A71918	probable secretion	809	692	2	A36143	phospholipase C (E
737	6	2.8	591	2	G90988	probable chaperoni	810	692	2	E83230	non-hemolytic phos
738	6	2.8	592	2	B83231	probable short-cha	811	695	2	E70923	hypothetical prote
739	6	2.8	592	2	D75421	conserved hypothet	812	698	2	S52696	myosin heavy chain
740	6	2.8	593	2	F95939	probable adenine d	813	698	2	T17261	hypothetical prote
741	6	2.8	593	2	H64594	multidrug resistanc	814	702	2	C71269	probable polyribon
742	6	2.8	595	2	A48658	flagellin - Escher	815	702	2	S12638	transposition prot
743	6	2.8	595	2	B48658	flagellin - Escher	816	704	1	S50448	1,4-alpha-glucan b
744	6	2.8	598	2	S55638	minor capsid prote	817	710	1	A46273	soluble lytic mure
745	6	2.8	600	2	D90155	hypothetical prote	818	710	2	G82689	probable fadE34 pr
746	6	2.8	601	2	T04747	hypothetical prote	819	711	2	C70606	gag protein - silk
747	6	2.8	604	2	S57065	probable membrane	820	712	2	T18195	NADH-ubiquinone ox
748	6	2.8	604	2	F72035	conserved hypothet	821	713	2	F82822	hypothetical prote
749	6	2.8	604	2	F86589	phenol 2-monooxyge	822	714	2	G75623	probable membrane
750	6	2.8	607	2	JQ1132	probable sodium/hy	823	715	2	S52675	hypothetical prote
751	6	2.8	611	2	G83177	SOX-3 protein - qu	824	716	2	G83612	probable copper-tr
752	6	2.8	613	2	JC7762	sulfite reductase	825	718	2	G70978	homeobox protein A
753	6	2.8	614	2	B82329	U1 snRNP 70K prote	826	718	2	T05850	protein kinase hom
754	6	2.8	614	2	A25707	conserved hypothet	827	719	2	T02154	hypothetical prote
755	6	2.8	616	2	C83404	proline-tRNA ligas	828	723	2	G84507	hypothetical prote
756	6	2.8	617	2	S75447	methylmalonyl-CoA	829	725	2	T00492	hypothetical prote
757	6	2.8	617	2	JC4559	hypothetical prote	830	727	2	T18600	hypothetical prote
758	6	2.8	617	2	F75484	transcription fact	831	727	2	AD1868	hypothetical prote
759	6	2.8	618	2	JC4366		832	731	2	I60729	ornithine decarbox

833	6	2.8	731	2	A98109	ornithine decarbox	906	6	2.8	898	2	D86122	Mg2+ transport ATP
834	6	2.8	731	2	D85954	ornithine decarbox	907	6	2.8	902	2	B57147	Mg2+-transporting
835	6	2.8	732	2	A40839	ornithine decarbox	908	6	2.8	902	2	AH1058	Mg(2+) transport A
836	6	2.8	732	2	A99719	ornithine decarbox	909	6	2.8	904	2	AH2019	hypothetical prote
837	6	2.8	732	2	A85569	ornithine decarbox	910	6	2.8	908	2	C70168	DNA polymerase I (
838	6	2.8	740	1	F0LJHD	gag polyprotein -	911	6	2.8	908	2	A93424	assimilatory nitra
839	6	2.8	741	2	D95966	probable aldehyde	912	6	2.8	911	2	T01353	probable serine/th
840	6	2.8	748	2	S59327	hypothetical prote	913	6	2.8	911	2	H97053	penicillin-binding
841	6	2.8	749	2	A70812	hypothetical glyci	914	6	2.8	912	2	D72644	hypothetical prote
842	6	2.8	757	2	S27762	Sip1 protein - bar	915	6	2.8	922	2	I37292	DNA ligase (ATP) (
843	6	2.8	759	2	A82052	two-component hybr	916	6	2.8	924	2	D81349	nitrate reductase
844	6	2.8	763	2	AC0108	probable primase Y	917	6	2.8	924	2	C83572	organic solvent to
845	6	2.8	765	2	S45033	probable imbibitio	918	6	2.8	931	2	S66574	transferrin-bindin
846	6	2.8	765	2	AF0118	probable kinase YP	919	6	2.8	932	1	VEBEC	glycoprotein g1 pr
847	6	2.8	767	2	E70895	hypothetical glyci	920	6	2.8	932	2	I52527	PACE4A - mouse (fr
848	6	2.8	768	2	S71477	homeotic protein,	921	6	2.8	932	2	T28820	hypothetical prote
849	6	2.8	768	2	H82367	sensory box/GGDPF	922	6	2.8	937	2	I53282	gene PACB4 protein
850	6	2.8	773	2	T46188	inhibition protein	923	6	2.8	940	2	S49087	lactoferrin-bindin
851	6	2.8	779	2	S57805	aconitate hydratase	924	6	2.8	943	2	G81070	lactoferrin-bindin
852	6	2.8	779	2	T21021	hypothetical prote	925	6	2.8	944	2	C81798	lactoferrin bindin
853	6	2.8	781	2	A43866	neuraminidase - VI	926	6	2.8	944	2	T18911	hypothetical prote
854	6	2.8	782	2	H95306	probable amino aci	927	6	2.8	948	2	C83060	hypothetical prote
855	6	2.8	783	2	A48998	nucleolar protein	928	6	2.8	950	1	S69704	hypothetical prote
856	6	2.8	784	2	E72515	probable DNA-direc	929	6	2.8	952	2	S64473	translation initia
857	6	2.8	787	2	A75347	GTP pyrophosphokin	930	6	2.8	953	2	S19427	probable membrane
858	6	2.8	788	2	C84616	similar to mammali	931	6	2.8	961	2	T23395	hypothetical prote
859	6	2.8	790	1	TVRHUTT	nerve growth facto	932	6	2.8	971	2	T32883	hypothetical prote
860	6	2.8	794	2	E90803	hypothetical prote	933	6	2.8	990	2	H86293	protein T24D18.4 [
861	6	2.8	795	2	A85612	hypothetical prote	934	6	2.8	993	2	S46779	26S proteasome reg
862	6	2.8	799	1	TVRTTB	nerve growth facto	935	6	2.8	994	2	A70776	probable glnE - My
863	6	2.8	799	2	C86287	F9L1.24 protein -	936	6	2.8	996	2	F86410	protein F3M18.12 [
864	6	2.8	802	1	A44223	DNA excision repai	937	6	2.8	1001	2	AG1979	hypothetical prote
865	6	2.8	802	2	A83125	probable TonB-depe	938	6	2.8	1013	2	A69226	type I restriction
866	6	2.8	803	2	I68600	dipeptidyl aminope	939	6	2.8	1014	2	AC1971	valyl-tRNA synthet
867	6	2.8	803	2	A41793	dipeptidyl aminope	940	6	2.8	1018	2	H83135	probable adhesin P
868	6	2.8	806	2	A41341	microbial serine p	941	6	2.8	1032	2	H87470	AcrrB/AcrD/AcrF fam
869	6	2.8	807	2	E82158	neuraminidase VC17	942	6	2.8	1043	2	H83329	probable RND efflu
870	6	2.8	812	2	AE3010	TonB-dependent rec	943	6	2.8	1044	2	F95375	probable drug resi
871	6	2.8	815	2	T00546	serine/threonine-s	944	6	2.8	1049	1	CG8078	collagen alpha 1(I
872	6	2.8	817	2	T22442	hypothetical prote	945	6	2.8	1050	2	JC7578	endo-1,4-beta-xyla
873	6	2.8	819	2	B47057	hypothetical kinase (946	6	2.8	1051	2	A38373	ubiquitin--protein
874	6	2.8	819	2	AH0056	aspartate kinase (947	6	2.8	1057	2	A42109	glycine dehydrogen
875	6	2.8	822	2	S19947	fibroblast growth	948	6	2.8	1076	1	A35622	nuclear pore prote
876	6	2.8	822	2	B49151	fibroblast growth	949	6	2.8	1077	2	B82566	acriflavin resista
877	6	2.8	824	2	F87330	photosynthesis pro	950	6	2.8	1083	2	A38919	hypothetical prote
878	6	2.8	825	2	A26983	regulatory protein	951	6	2.8	1089	2	S53978	PSEL protein - yea
879	6	2.8	830	2	T18860	hypothetical prote	952	6	2.8	1091	2	T34107	hypothetical prote
880	6	2.8	831	2	A48489	nitrate reductase	953	6	2.8	1096	1	S61917	protein kinase C (
881	6	2.8	831	2	S50163	nitrate reductase	954	6	2.8	1099	2	A59311	myosin VIII, 2MK3
882	6	2.8	832	2	A31246	neurogenic protein	955	6	2.8	1116	2	B88612	protein Y76A2A.2 [
883	6	2.8	833	2	S19087	gene Delta protein	956	6	2.8	1117	2	C91286	hypothetical prote
884	6	2.8	833	2	A96274	probable tonB-depe	957	6	2.8	1117	2	G86127	hypothetical prote
885	6	2.8	834	2	A97178	probable permease	958	6	2.8	1131	2	A23944	chitin synthase (E
886	6	2.8	835	2	F72624	probable cation-tr	959	6	2.8	1133	2	T01920	probable RNA-direc
887	6	2.8	838	2	S23606	potassium channel	960	6	2.8	1147	1	MWAXIB	myosin heavy chain
888	6	2.8	839	2	A56337	glycoprotein phosp	961	6	2.8	1154	2	T48829	related to SREBP c
889	6	2.8	841	2	F81172	DNA ligase NMB0666	962	6	2.8	1155	2	G96539	hypothetical prote
890	6	2.8	853	2	B85429	beta-galactosidase	963	6	2.8	1156	2	T14899	aminophospholipid
891	6	2.8	853	2	T04600	probable beta-gala	964	6	2.8	1166	1	S06142	protein-tyrosine k
892	6	2.8	855	2	A48168	proliferating-cell	965	6	2.8	1166	2	S33812	myosin-like protei
893	6	2.8	857	2	S62694	potassium channel	966	6	2.8	1166	2	T13958	myosin-b1 protein
894	6	2.8	862	2	A96778	hypothetical prote	967	6	2.8	1174	1	H3BYDH	helicase (EC 3.6.1
895	6	2.8	865	2	I54331	dipeptidyl aminope	968	6	2.8	1179	2	H82706	hypothetical prote
896	6	2.8	880	2	S00670	neurogenic repetit	969	6	2.8	1181	2	A43346	1-phosphatidylino
897	6	2.8	886	2	I50694	collagen alpha 1(I	970	6	2.8	1186	2	S61647	probable membrane
898	6	2.8	886	2	S07132	hypothetical prote	971	6	2.8	1187	2	T20544	hypothetical prote
899	6	2.8	889	2	A35989	modulation protein	972	6	2.8	1196	2	S40908	TyB protein - yea
900	6	2.8	891	2	B82495	probable NADH dehy	973	6	2.8	1207	2	T16011	hypothetical prote
901	6	2.8	892	2	T09193	ataxin 7 - human	974	6	2.8	1213	2	T19835	hypothetical prote
902	6	2.8	893	2	T35014	probable regulator	975	6	2.8	1228	2	AE2397	protoporphyrin IX
903	6	2.8	894	2	B65557	probable receptor	976	6	2.8	1231	2	C84716	hypothetical prote
904	6	2.8	898	2	E65236	Mg(2+) transport A	977	6	2.8	1237	2	T14633	hypothetical prote
905	6	2.8	898	2	C91281	Mg2+ transport ATP	978	6	2.8	1238	1	JC5573	copper-transportin

```
979      6      2.8      1238      2      T40120
980      6      2.8      1249      2      C83358
981      6      2.8      1249      2      T14270
982      6      2.8      1263      2      T00649
983      6      2.8      1265      1      A37967
984      6      2.8      1273      2      E72611
985      6      2.8      1278      2      B22671
986      6      2.8      1290      2      A56493
987      6      2.8      1293      2      T14259
988      6      2.8      1298      2      T47523
989      6      2.8      1300      2      T18364
990      6      2.8      1328      2      S52481
991      6      2.8      1328      2      S52894
992      6      2.8      1328      2      S50948
993      6      2.8      1328      2      B22999
994      6      2.8      1328      2      B28097
995      6      2.8      1339      2      A55301
996      6      2.8      1339      2      G84764
997      6      2.8      1341      2      S66835
998      6      2.8      1356      2      F84486
999      6      2.8      1356      2      T18754
1000     6      2.8      1379      2      T45119

C2H2 type zinc fin
probable non-ribos
Ras-GTPase activat
hypothetical prote
neural cell adhesi
probable ATP-depen
Tyb protein - years
leucocyte common a
ras GTPase-activat
DNA-binding protei
ro-3 protein - Neu
Tyb protein - years
Tyb protein - years
Tyb protein - years
Tyb protein - years
1,3-beta-D-glucan-
hypothetical prote
probable membrane
probable retroelem
hypothetical prote
FIM protein (impor

ALIGNMENTS

RESULT 1
JC7353
fibroblast growth factor-20 - human
C:Species: Homo sapiens (man)
C:Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 01-Dec-2000
C:Accession: JC7353
R:Kirkoshi, H.; Sagara, N.; Saitoh, T.; Tanaka, K.; Sekihara, H.; Shiohara, K.; Katoh,
Biochem. Biophys. Res. Commun. 274, 337-343, 2000
A:Title: Molecular cloning and characterization of human FGF-20 on chromosome 8p21.3-p22
A:Reference number: JC7353
A:Accession: JC7353
A:Molecule type: mRNA
A:Residues: 1-211 <KIR>
A:Cross-references: DDBJ:AB044277
C:Comment: This factor is involved in physiological and pathological processes, playing
C:Genetics:
A:Map position: 8p21.3-8p22
A:Superfamily: fibroblast growth factor
C:Keywords: angiogenesis; carcinogenesis

Query Match 100.0%; Score 211; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.7e-213;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAPLAEVGGFLGGLEGGLQQVGSFHLPPAGERPPLLGERRSAERSARGGPGAAQLAHL 60
Db 1 MAPLAEVGGFLGGLEGGLQQVGSFHLPPAGERPPLLGERRSAERSARGGPGAAQLAHL 60

Qy 61 HGIILRRQLYCRGTGFHLQILPDGVSQVQCTRODHSLEFISVAVGLVSRGVDGSLYLG 120
Db 61 HGIILRRQLYCRGTGFHLQILPDGVSQVQCTRODHSLEFISVAVGLVSRGVDGSLYLG 120

Qy 121 MNDKGLYGSSEKLTSECFRQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTTPRDGAR 180
Db 121 MNDKGLYGSSEKLTSECFRQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTTPRDGAR 180

Qy 181 SKRHQKTFHFLPRVDPVDPVPELYKDLLMYT 211
Db 181 SKRHQKTFHFLPRVDPVDPVPELYKDLLMYT 211

RESULT 2
JC7511
fibroblast growth factor-20 - rat
C:Species: Rattus norvegicus (Norway rat)
```

```
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: JC7511
R:Ohmachi, S.; Watanabe, Y.; Mikami, T.; Kusu, N.; Ibi, T.; Akaike, A.; Itoh, N.
Biochem. Biophys. Res. Commun. 277, 355-360, 2000
A:Title: FGF-20, a novel neurotrophic factor, preferentially expressed in the substan
A:Reference number: JC7511; MUID:20490008
A:Contents: Brain
A:Accession: JC7511
A:Molecule type: DNA
A:Residues: 1-212 <OHM>
A:Cross-references: DDBJ:AB020021
C:Comment: This factor is secreted, and plays an important role as a neurotrophic fac
C:Genetics:
A:Gene: fgf-20
C:Keywords: brain; growth factor; neurotrophic factor

Query Match 40.3%; Score 85; DB 2; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.5e-81;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 KGELYGSEKLTSECFRQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTTPRDGARSKR 183
Db 124 KGELYGSEKLTSECFRQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTTPRDGARSKR 183

Qy 184 HQKFTHFLPRVDPVDPVPELYKDLL 208
Db 184 HQKFTHFLPRVDPVDPVPELYKDLL 208

RESULT 3
JC7082
fibroblast somatotropin-20 - African clawed frog
N:Alternate names: fibroblast growth factor-20
C:Species: Xenopus laevis (African clawed frog)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: JC7082
R:Koga, C.; Adati, N.; Nakata, K.; Mikoshiba, K.; Furuhata, Y.; Sato, S.; Tei, H.; Sa
Biochem. Biophys. Res. Commun. 261, 756-765, 1999
A:Title: Characterization of a novel member of the FGF family, XFGF-20, in Xenopus la
A:Reference number: JC7082; MUID:99373151
A:Accession: JC7082
A:Molecule type: mRNA
A:Residues: 1-208 <KOG>
A:Cross-references: DDBJ:AB012615; NID:g5762261; PIDN:BAA83474.1; PID:g5762262
C:Superfamily: fibroblast growth factor
C:Keywords: differentiation; fibroblast; growth factor; heparin binding

Query Match 12.3%; Score 26; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 3.1e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 129 GSEKLTSECFRQFEENWNTYSSN 154
Db 126 GSEKLTSECFRQFEENWNTYSSN 151

RESULT 4
S66486
fibroblast growth factor 9 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S66486
R:Seo, M.; Noguchi, K.
FEBS Lett. 370, 231-235, 1995
A:Title: Retinoic acid induces gene expression of fibroblast growth factor-9 during i
A:Reference number: S66486; MUID:95385801
A:Accession: S66486
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-208 <SEO>
A:Cross-references: EMBL:D38258; NID:g1107458; PIDN:BAA07410.1; PID:g1107459
C:Superfamily: fibroblast growth factor
```

```
Query Match          9.0%; Score 19; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 6.9e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVSRGVDSGLYLGMN 122
Db 101 AVGLVSRGVDSGLYLGMN 119

RESULT 5
A48137
fibroblast growth factor 9 - human
N:Alternate names: glia-activating factor
C:Species: Homo sapiens (man)
C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: A48137
R: Miyamoto, M.; Naruo, K.; Seko, C.; Matsumoto, S.; Kondo, T.; Kurokawa, T.
Mol. Cell. Biol. 13, 4251-4259, 1993
A: Title: Molecular cloning of a novel cytokine cDNA encoding the ninth member of the fib
A: Reference number: A48137; MUID: 93309459
A: Accession: A48137
A: Status: preliminary
A: Molecule type: nucleic acid
A: Residues: 1-208 <MIY>
A: Cross-references: GB: D14836; NID: g391718; PIDN: BAA03572.1; PID: g391719
A: Experimental source: forestin
A: Note: sequence extracted from NCBI backbone (NCBIN: 134640, NCBIPI: 134641)
C: Genetics:
A: Gene: GDB: FGF9
A: Cross-references: GDB: 207221; OMIM: 600921
A: Map position: 13q11-13q12
C: Superfamily: fibroblast growth factor

Query Match          9.0%; Score 19; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 6.9e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVSRGVDSGLYLGMN 122
Db 101 AVGLVSRGVDSGLYLGMN 119

RESULT 6
JC5940
fibroblast growth factor 16 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: JC5940
R: Miyake, A.; Konishi, M.; Martin, F.H.; Hernday, N.A.; Ozaki, K.; Yamamoto, S.; Mikami,
Biochem. Biophys. Res. Commun. 243, 148-152, 1998
A: Title: Structure and expression of a novel member, FGF-16, of the fibroblast growth fa
A: Reference number: JC5940; MUID: 98139883
A: Accession: JC5940
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-207 <MIY>
A: Cross-references: DDBJ: AB002561; NID: g29111149; PIDN: BAA24947.1; PID: g2911150
C: Superfamily: fibroblast growth factor

Query Match          7.6%; Score 16; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 9.7e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 GILRRRLQYCRGTGPHL 77
Db 58 GILRRRLQYCRGTGPHL 73

RESULT 7
JC5941
fibroblast growth factor 16 - human
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
```

```
C:Accession: JC5941
R: Miyake, A.; Konishi, M.; Martin, F.H.; Hernday, N.A.; Ozaki, K.; Yamamoto, S.; Mika
Biochem. Biophys. Res. Commun. 243, 148-152, 1998
A: Title: Structure and expression of a novel member, FGF-16, of the fibroblast growth
A: Reference number: JC5940; MUID: 98139883
A: Accession: JC5941
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-207 <MIY>
A: Cross-references: DDBJ: AB009391; NID: g29111169; PIDN: BAA24956.1; PID: g2911170
C: Superfamily: fibroblast growth factor

Query Match          7.6%; Score 16; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 9.7e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 GILRRRLQYCRGTGPHL 77
Db 58 GILRRRLQYCRGTGPHL 73

RESULT 8
E69134
conserved hypothetical protein MTH273 - Methanobacterium thermoautotrophicum (strain
C:Species: Methanobacterium thermoautotrophicum
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Sep-1999
C:Accession: E69134
R: Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A: Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu
A: Reference number: A69000; MUID: 98037514
A: Accession: E69134
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-151 <MTH>
A: Cross-references: GB: AE000813; GB: AE000666; NID: g2621320; PIDN: AAB84779.1; PID: g262
A: Experimental source: strain Delta H
C: Genetics:
A: Gene: MTH273
C: Superfamily: conserved hypothetical protein ybhB

Query Match          3.8%; Score 8; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 LPDGSVQG 87
Db 80 LPDGSVQG 87

RESULT 9
G87417
conserved hypothetical protein CC1358 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C:Accession: G87417
R: Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
n.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A: Title: Complete Genome Sequence of Caulobacter crescentus.
A: Reference number: AB7249; MUID: 21173698; PMID: 11259647
A: Accession: G87417
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-157 <STO>
A: Cross-references: GB: AE005673; NID: g13422709; PIDN: AAK23339.1; GSPDB: GN00148
C: Genetics:
A: Gene: CC1358
C: Superfamily: conserved hypothetical protein HI0943
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Query Match          3.8%; Score 8; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 RPVDPERV 200
Db 77 RPVDPERV 84

RESULT 10
A86430
F26G16.12 protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
R:Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
ansen, N.F.; Hughes, B.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Lin, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: A86430
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-197 <STO>
A:Cross-references: GB:AE005172; NID:g6634774; PIDN:AAF19754.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match          3.8%; Score 8; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 HGILRRRQ 68
Db 117 HGILRRRQ 124

RESULT 11
T01363
hypothetical protein At2g34720 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein T29F13.7
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-2001
C:Accession: T01363; B84760
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, May 1998
A:Description: Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence.
A:Reference number: 214179
A:Accession: T01363
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-226 <ROU>
A:Cross-references: EMBL:AC003096; NID:g3132469; PID:g3132473
A:Experimental source: cultivar Columbia
A:Note: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umavam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: B84760
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-226 <STO>
A:Cross-references: GB:AE002093; NID:g3132473; PIDN:AAC16262.1; GSPDB:GN00139
C:Genetics:

A:Gene: At2g34720; T29F13.7
A:Map position: 2
A:Introns: 44/3; 76/3; 104/3; 159/3

Query Match          3.8%; Score 8; DB 2; Length 226;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 HGILRRRQ 68
Db 136 HGILRRRQ 143

RESULT 12
T45935
probable galactose oxidase (EC 1.1.3.9) F5K20.250 [similarity] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 24-Oct-2000
C:Accession: T45935
R:Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Mewes, H.W.; Lemcke, K.; Mayer, K.F
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23017
A:Accession: T45935
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-545 <MON>
A:Cross-references: EMBL:ALJ32960
A:Experimental source: cultivar Columbia; BAC clone F5K20
C:Genetics:
A:Map position: 3
A:Note: F5K20.250
C:Superfamily: Arabidopsis thaliana hypothetical protein F5K20.250
C:Keywords: copper; metal binding; oxidoreductase
F:116-168/Cross-link: cysteinyltyrosine (Cys-Tyr) #status predicted
F:168,390,391,483/Binding site: copper (Tyr, Tyr, His, His) #status predicted

Query Match          3.8%; Score 8; DB 2; Length 545;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 QILPDGSV 85
Db 172 QILPDGSV 179

RESULT 13
F59092
hypothetical protein pX01-14 - Bacillus anthracis virulence plasmid pX01
C:Species: Bacillus anthracis
C:Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 11-May-2000
C:Accession: F59092
R:Oknaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koeh
J. Bacteriol. 181, 6509-6515, 1999
A:Title: Sequence and organization of pX01, the large Bacillus anthracis plasmid harb
A:Reference number: A59091; MUID:99445483
A:Accession: F59092
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-564 <OKI>
A:Cross-references: GB:AF065404; NID:g4894216; PIDN:AAD32318.1; PID:g4894230
A:Experimental source: strain Sterne
C:Genetics:
A:Gene: pX01-14
A:Genome: plasmid
C:Superfamily: Bacillus anthracis virulence plasmid pX01 hypothetical protein pX01-14

Query Match          3.8%; Score 8; DB 2; Length 564;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 LYGSEKLT 134
Db 329 LYGSEKLT 336
```

```
RESULT 14
T00367
hypothetical protein KIAA0665 - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C:Accession: T00367
R:Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.
DNA Res. 5, 169-176, 1998
A:Title: Prediction of the coding sequences of unidentified human genes. X. The complete
A:Reference number: Z14142; MUID:98403880
A:Accession: T00367
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-756 <ISH>
A:Cross-references: EMBL:AB014565; NID:g3327143; PIDN:BAA31640.1; PID:g3327144
A:Experimental source: brain
C:Genetics:
A:Note: KIAA0665

Query Match          3.8%; Score 8; DB 2; Length 756;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GPGAAQLA 58
      |||||
Db 26 GPGAAQLA 33

RESULT 15
T42229
probable E1-E2 ATPase (EC 3.6.1.-) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
C:Accession: T42229
R:Halleck, M.S.; Blackman, C.F.; Gao, L.; Williamson, P.L.; Schlegel, R.A.
submitted to the EMBL Data Library, June 1997
A:Description: Multiple members of a third subfamily of P-type ATPases identified by gen
A:Reference number: Z22089
A:Accession: T42229
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1020 <HAL>
A:Cross-references: EMBL:AF011336; NID:g2944186; PID:g2944187; PIDN:AAC05245.1
C:Keywords: hydrolase; transmembrane protein

Query Match          3.8%; Score 8; DB 2; Length 1020;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 PELYKDLL 208
      |||||
Db 880 PELYKDLL 887

Search completed: October 21, 2002, 16:21:25
Job time : 67 secs
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OM protein - protein search, using sw model

Run on: October 21, 2002, 16:15:41 ; Search time 13 seconds

(without alignments)

628.448 Million cell updates/sec

Title: US-09-817-814-2

Perfect score: 211

Sequence: 1 MAPLAEVGGFGLGLEGLGQQ.....PRPVDPRVPELYKDLIMYT 211

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	211	100.0	211	1	FGFK_HUMAN
2	20	9.5	209	1	FGF9_XENLA
3	19	9.0	208	1	FGF9_HUMAN
4	19	9.0	208	1	FGF9_MOUSE
5	19	9.0	208	1	FGF9_RAT
6	16	7.6	207	1	FGFG_HUMAN
7	16	7.6	207	1	FGFG_RAT
8	8	3.8	151	1	Y273_METTH
9	8	3.8	157	1	YD58_CAUCR
10	8	3.8	756	1	Y665_HUMAN
11	8	3.8	1047	1	AT2A_HUMAN
12	8	3.8	1047	1	AT9A_MOUSE
13	7	3.3	94	1	THEB_HAEIN
14	7	3.3	120	1	CERPL_CERPI
15	7	3.3	142	1	GLBI_LUMTE
16	7	3.3	155	1	RS11_YEAST
17	7	3.3	232	1	HXA6_MOUSE
18	7	3.3	242	1	GSHV_ARATH
19	7	3.3	246	1	MYPO_HETFR
20	7	3.3	252	1	BPE4_HUMAN
21	7	3.3	262	1	PLCL1_CAEEL
22	7	3.3	337	1	AT9B_HUMAN
23	7	3.3	391	1	RRPP_MUMPE
24	7	3.3	391	1	RRPP_MUMPM
25	7	3.3	409	1	CAD1_YEAST
26	7	3.3	413	1	L756_CAEEL
27	7	3.3	415	1	BOFH_BRAOL
28	7	3.3	423	1	DHE3_AERPE
29	7	3.3	424	1	LFY_ARATH
30	7	3.3	426	1	TOLB_CHLMU
31	7	3.3	431	1	TOLB_CHLTM
32	7	3.3	460	1	COAA_BP1F1
33	7	3.3	492	1	VHS_HSV2G

34	7	3.3	511	1	IE63_HSV1E
35	7	3.3	512	1	IE63_HSV1I
36	7	3.3	626	1	TESK_HUMAN
37	7	3.3	627	1	TESK_MOUSE
38	7	3.3	628	1	TESK_RAT
39	7	3.3	695	1	TRFL_HORSE
40	7	3.3	708	1	TRFL_CAMDR
41	7	3.3	709	1	MBA2_ECOLI
42	7	3.3	711	1	TRFL_HUMAN
43	7	3.3	739	1	PSAA_SYNPO
44	7	3.3	863	1	IMBI_SCHP2
45	7	3.3	1095	1	AT9B_MOUSE
46	7	3.3	1128	1	DNBI_EBV
47	7	3.3	1856	1	MGA_HUMAN
48	7	3.3	3390	1	POLG_DEN3
49	7	3.3	4303	1	PKDI_HUMAN
50	6	2.8	31	1	PETL_ODOSI
51	6	2.8	57	1	SMS2_PTIAME
52	6	2.8	68	1	MRSA_BACSP
53	6	2.8	78	1	HOLI_BPHPI
54	6	2.8	107	1	URE2_BACSB
55	6	2.8	114	1	PTI3_STYPL
56	6	2.8	118	1	NLT6_AMBAR
57	6	2.8	118	1	YUSI_BACSU
58	6	2.8	123	1	NEF_HV1B1
59	6	2.8	123	1	NEF_HV1H2
60	6	2.8	123	1	URE2_UREPA
61	6	2.8	123	1	URE2_UREUR
62	6	2.8	124	1	LEG_BACSU
63	6	2.8	129	1	LEG_ELEEL
64	6	2.8	135	1	IF2B_METTH
65	6	2.8	141	1	GLB_TUBTU
66	6	2.8	141	1	HBAL_NAJNA
67	6	2.8	143	1	YG32_VZVD
68	6	2.8	143	1	YW84_MYCTU
69	6	2.8	144	1	URE2_YERPE
70	6	2.8	145	1	DFP_STRMU
71	6	2.8	145	1	VG46_BPMU
72	6	2.8	146	1	Y4JN_RHISN
73	6	2.8	149	1	CABO_LOLPE
74	6	2.8	151	1	ARGR_HAEIN
75	6	2.8	152	1	RT16_CAEEL
76	6	2.8	154	1	YK01_AERPE
77	6	2.8	155	1	ARGR_PASMU
78	6	2.8	156	1	ARGR_ECOLI
79	6	2.8	156	1	ARGR_SALTY
80	6	2.8	161	1	VANZ_ENTFC
81	6	2.8	163	1	URE2_YEREN
82	6	2.8	174	1	PUR6_MYCTU
83	6	2.8	178	1	VEGA_MYXXA
84	6	2.8	180	1	NEF_HV2NZ
85	6	2.8	183	1	KADA_THEAC
86	6	2.8	186	1	MAUE_PARDE
87	6	2.8	187	1	FGFA_XENLA
88	6	2.8	188	1	FGF9_MFTJA
89	6	2.8	192	1	FGFB_XENLA
90	6	2.8	194	1	FGFA_CHICK
91	6	2.8	199	1	TBP_PYROC
92	6	2.8	202	1	FGF4_MOUSE
93	6	2.8	205	1	NEF_HV1B8
94	6	2.8	205	1	NEF_HV1S3
95	6	2.8	205	1	NEF_SIVCZ
96	6	2.8	206	1	FGF4_BOVIN
97	6	2.8	206	1	FGF4_HUMAN
98	6	2.8	206	1	NEF_HV1I2
99	6	2.8	206	1	NEF_HV1BR
100	6	2.8	206	1	NEF_HV1EL
101	6	2.8	206	1	NEF_HV1LW
102	6	2.8	206	1	NEF_HV1PV
103	6	2.8	207	1	NEF_HV1ND
104	6	2.8	207	1	Y214_MYCGE
105	6	2.8	208	1	FGF6_HUMAN
106	6	2.8	208	1	FGF6_MOUSE

P36295	herpes simp
P10238	herpes simp
Q15569	homo sapien
Q70146	mus musculus
Q63572	rattus norv
Q77811	equus cabal
Q9TUM0	canamelus dro
P07112	escherichia
P02788	homo sapien
P17154	synecococc
Q13864	schizosacch
P98195	mus musculus
P03227	epstein-bar
Q43451	homo sapien
P27915	d genome po
P98161	homo sapien
P49524	odontella s
P81879	piaractus m
P43683	bacillus sp
P51727	bacterioph
Q07398	bacillus sp
P28205	steyela plic
Q04004	ambrosia ar
Q32175	bacillus su
P03404	human immun
P04601	human immun
Q56558	ureaplasma
P17273	ureaplasma
P71035	electrophor
P08520	electrophor
Q27797	methanobact
P18202	tubifex tub
Q9PR19	naja naja (
P09285	varicella-z
P96889	mycobacteri
P52314	versinia pe
Q54433	streptococc
Q9TIV3	bacterioph
P55514	rhizobium s
P45333	lolligo peal
P45110	haemophilus
Q10129	caenorhabdi
Q9VAD8	aeropyrum p
P57850	pasteurella
P15282	escherichia
P37170	salmonella
Q06242	enterococcu
P31495	versinia en
P96880	mycobacteri
P07935	myxococcus
P05860	human immun
Q9H1I1	thermoplasm
P29896	paracoccus
P48805	xenopus lae
Q58954	methanococc
P48806	xenopus lae
P48804	gallus gall
P58177	pyrodictium
P11403	mus musculus
P05855	human immun
P19545	human immun
P17664	chimpanzee
P48803	bos taurus
P08620	homo sapien
P04324	human immun
P03406	human immun
P04604	human immun
Q70627	human immun
P03405	human immun
P18801	human immun
P47456	mycoplasma
P10767	homo sapien
P21658	mus musculus

107	1	NEF_HV1S1	208	2.8	6	180	1	TF2B_ARCFU	326	1	archaeoglob
108	1	NEF_HV1A2	210	2.8	6	181	1	Y083_CAUCR	326	1	caulobacter
109	1	NEF_HV1O2	211	2.8	6	182	1	APA2_KLULA	331	1	kluyveromyc
110	1	NEF_HV1Z6	212	2.8	6	183	1	TAL_HUMAN	331	1	homo sapien
111	1	URE1_HELW2	213	2.8	6	184	1	SIX3_HUMAN	332	1	homo sapien
112	1	YKGB_HAEIN	213	2.8	6	185	1	SIX3_MOUSE	333	1	mus musculus
113	1	NEF_HV1Y2	214	2.8	6	186	1	HXDB_HUMAN	338	1	homo sapien
114	1	NEF_HV1JR	216	2.8	6	187	1	YDDR_ECOLI	340	1	escherichia
115	1	GTM1_HUMAN	217	2.8	6	188	1	RTCA_PYRAB	342	1	pyroctococ
116	1	GTM2_HUMAN	217	2.8	6	189	1	DDL_STRPN	347	1	streptococ
117	1	GTM3_MOUSE	217	2.8	6	190	1	VAL1_PHVU	349	1	pepper huas
118	1	LIPB_PASMU	218	2.8	6	191	1	R51B_MOUSE	350	1	mus musculus
119	1	NEF_HV1BN	218	2.8	6	192	1	VAL1_TGMV	352	1	tomato gold
120	1	TPIS_CHLAU	220	2.8	6	193	1	VAL1_BGMV	353	1	bean golden
121	1	YD41_MYCLE	220	2.8	6	194	1	MAT1_COCCY	354	1	cochliobolu
122	1	SCRK_SALTH	221	2.8	6	195	1	VAL1_ABMVW	355	1	abutilon mo
123	1	YUG4_CABEL	223	2.8	6	196	1	CCDA_CABEL	356	1	caenorhabdi
124	1	2313_HUMAN	228	2.8	6	197	1	VAL1_TYLCV	357	1	tomato yell
125	1	CLD2_CANFA	230	2.8	6	198	1	PE22_HUMAN	358	1	homo sapien
126	1	CLD2_HUMAN	230	2.8	6	199	1	VAL1_BCTV	358	1	beet curly
127	1	CLD2_MOUSE	231	2.8	6	200	1	VAL1_CLVK	358	1	cassava lat
128	1	VHEL_CVB	231	2.8	6	201	1	VAL1_CLVN	358	1	cassava lat
129	1	YE14_YEAST	231	2.8	6	202	1	VAL1_TYLCM	359	1	tomato yell
130	1	URE1_HELRE	234	2.8	6	203	1	VAL1_TYLCU	359	1	tomato yell
131	1	ABME_RABIT	236	2.8	6	204	1	WNT2_HUMAN	360	1	homo sapien
132	1	MLPA_MYXXA	236	2.8	6	205	1	WNT2_MOUSE	360	1	mus musculus
133	1	UBL1_YEAST	236	2.8	6	206	1	VAL1_PYMV	361	1	potato yell
134	1	URE1_HELFE	237	2.8	6	207	1	VAL1_TMOV	361	1	tomato mott
135	1	2198_MOUSE	237	2.8	6	208	1	VAL1_TYLCV	362	1	tomato yell
136	1	IAH1_YEAST	238	2.8	6	209	1	NMPC_ECOLI	365	1	escherichia
137	1	CMF1_YEAST	239	2.8	6	210	1	POR1_BPPA2	365	1	bacterioph
138	1	NEF_HV1SC	239	2.8	6	211	1	GCST_MYCLE	367	1	mycobacteri
139	1	PYRF_HALN1	242	2.8	6	212	1	GCST_MYCTU	367	1	mycobacteri
140	1	RECO_ECOLI	242	2.8	6	213	1	AROC_BACSU	368	1	bacillus su
141	1	RECO_SALTY	242	2.8	6	214	1	DAPE_CORGL	369	1	corynebacte
142	1	Y027_CABEL	243	2.8	6	215	1	CYB_EPIAN	370	1	epirates a
143	1	ARC3_CBCP	244	2.8	6	216	1	CYB_EPIFO	370	1	epirates f
144	1	T2P7_PSEAE	245	2.8	6	217	1	CYB_EPISU	370	1	epirates s
145	1	AXIB_ARATH	246	2.8	6	218	1	CYB_EUNNU	370	1	eunectes mu
146	1	NEF_HV2ST	255	2.8	6	219	1	CYB_EUNNO	370	1	eunectes no
147	1	UNG_HSV6U	255	2.8	6	220	1	CYB_ANISC	371	1	anilius scy
148	1	UNG_HSV62	255	2.8	6	221	1	CYB_EPIMO	371	1	epirates m
149	1	Y884_CABEL	255	2.8	6	222	1	CYB_ERVEL	371	1	eryx elega
150	1	NEF_HV2CA	260	2.8	6	223	1	CYB_ERIJA	371	1	eryx jaculu
151	1	BPHF_SPHAR	262	2.8	6	224	1	CYB_ERYMI	371	1	eryx miliar
152	1	FGF5_MOUSE	264	2.8	6	225	1	CYB_ERYMN	371	1	eryx miliar
153	1	YCJR_ECOLI	265	2.8	6	226	1	CYB_ERYTA	371	1	eryx tatar
154	1	FGF5_RAT	266	2.8	6	227	1	CYB_LATCO	371	1	laticauda c
155	1	FGF5_HUMAN	268	2.8	6	228	1	AGI_URTDI	372	1	urtica dioi
156	1	GS80_BACSU	273	2.8	6	229	1	RGSX_BOVIN	374	1	bos taurus
157	1	D101_ARATH	276	2.8	6	230	1	YY10_MYCTU	375	1	mycobacteri
158	1	TRPC_PSEPU	277	2.8	6	231	1	OMPC_SERMA	376	1	serratia ma
159	1	ILVE_METUA	288	2.8	6	232	1	RUL7_MOUSE	378	1	mus musculu
160	1	PDXK_SALTY	288	2.8	6	233	1	GRK1_ECOLI	381	1	escherichia
161	1	TEDR_ALCEU	288	2.8	6	234	1	RODA_HELPY	381	1	helicobacte
162	1	YF23_HAEIN	296	2.8	6	235	1	Y987_METTH	383	1	methanobact
163	1	CYB_PLAGA	300	2.8	6	236	1	CTRA_NEIMA	387	1	neisseria m
164	1	NORF_ALTHA	303	2.8	6	237	1	AROC_STAAU	388	1	staphylococ
165	1	NORF_COLMA	303	2.8	6	238	1	S17P_CHLRE	389	1	chlamydomon
166	1	NORF_PHOPO	303	2.8	6	239	1	CTRA_NEIMB	391	1	neisseria m
167	1	NORF_SHEHA	303	2.8	6	240	1	UVSX_BPT4	391	1	bacterioph
168	1	NORF_VIBMA	303	2.8	6	241	1	SPER_SCHPO	394	1	schizosacch
169	1	NORF_VIBPA	303	2.8	6	242	1	AXP_YARLI	397	1	yarrowia li
170	1	NORF_VIBPS	304	2.8	6	243	1	YEDS_ECOLI	397	1	escherichia
171	1	PTFB_BACAM	304	2.8	6	244	1	RL3_CABEL	401	1	caenorhabdi
172	1	SCRK_SALTY	307	2.8	6	245	1	CHEB_TREPA	403	1	treponema p
173	1	CNO7_CABEL	310	2.8	6	246	1	NQRE_NEIMA	405	1	neisseria m
174	1	K1PF_ECOLI	312	2.8	6	247	1	NQRE_NEIMB	405	1	neisseria m
175	1	EBAG_STRPL	313	2.8	6	248	1	NQRF_PASMU	407	1	pasteurella
176	1	K1PF_HAEIN	313	2.8	6	249	1	NQRF_VIBAL	407	1	v na(+)-tra
177	1	ATPG_SYNTP6	316	2.8	6	250	1	NQRF_VIBH	407	1	vibro harv
178	1	RCN2_HUMAN	317	2.8	6	251	1	NQRF_VIBCH	408	1	vibrio chol
179	1	HXDB_MOUSE	323	2.8	6	252	1	NER1_MOUSE	409	1	mus musculu

253	1	NER1_RAT	409	2.8	6	Q99pw3	rattus norv
254	1	NORF_HAEIN	411	2.8	6	O05012	haemophilus
255	1	GLYA_BACHD	413	2.8	6	Q9K694	bacillus su
256	1	QYH_BACSU	414	2.8	6	P54545	bacillus su
257	1	NER1_HUMAN	415	2.8	6	Q95119	homo sapien
258	1	EPF2_RALSO	418	2.8	6	O45412	raistonia s
259	1	PGK_TREPA	419	2.8	6	O83549	treponema p
260	1	SYS_MYCTU	419	2.8	6	P96244	mycobacteri
261	1	APEB_MYCLE	426	2.8	6	Q50022	mycobacteri
262	1	GLAI_MYCTU	426	2.8	6	O53441	mycobacteri
263	1	GLYA_MYCLE	426	2.8	6	Q9X794	mycobacteri
264	1	AROA_BUCAI	427	2.8	6	P57396	buchnera ap
265	1	TRBL_AERPE	427	2.8	6	Q9Y8T5	aeropyrum p
266	1	OM47_PASMU	428	2.8	6	P80603	pasteurella
267	1	AG45_MYCLE	429	2.8	6	P46838	mycobacteri
268	1	URAA_ECOLI	429	2.8	6	P33780	escherichia
269	1	PYRP_BACCL	432	2.8	6	P41006	bacillus ca
270	1	APEB_MYCTU	433	2.8	6	O06634	mycobacteri
271	1	ENO_BORBU	433	2.8	6	O51312	borrelia bu
272	1	PYRP_BACSU	434	2.8	6	P39766	bacillus su
273	1	RUI17_HUMAN	437	2.8	6	P08621	homo sapien
274	1	PHT3_PSEPU	439	2.8	6	Q05183	pseudomonas
275	1	SNDH_ACELI	449	2.8	6	Q44091	acetobacter
276	1	TBG_ENTHI	451	2.8	6	P54401	entamoeba h
277	1	MUC_SUNMU	457	2.8	6	P20768	suncus muri
278	1	VSG2_TRYEQ	457	2.8	6	P20950	trypanosoma
279	1	MERA_SERMA	460	2.8	6	P08662	seriatia ma
280	1	ANFK_AZOVI	462	2.8	6	P16267	azotobacter
281	1	YI02_MYCTU	463	2.8	6	O53951	mycobacteri
282	1	AAK1_PIG	464	2.8	6	Q9mnp4	sus scrofa
283	1	EXSH_RHIME	465	2.8	6	O33680	rhizobium m
284	1	VP19_HSV11	465	2.8	6	P32888	herpes simp
285	1	VP19_HSV14	465	2.8	6	P17586	herpes simp
286	1	VP19_HSV2G	466	2.8	6	P22486	herpes simp
287	1	CPXR_RHISN	467	2.8	6	P55543	rhizobium s
288	1	IRF6_HUMAN	467	2.8	6	O14896	homo sapien
289	1	IRF6_MOUSE	467	2.8	6	P97431	mus musculus
290	1	ERIC_EGO57	473	2.8	6	P58244	escherichia
291	1	ERIC_ECOLI	473	2.8	6	P37019	escherichia
292	1	RRG1_XENLA	476	2.8	6	P51127	xenopus lae
293	1	GAT2_HUMAN	480	2.8	6	P23769	homo sapien
294	1	GAT2_MOUSE	480	2.8	6	O09100	mus musculus
295	1	YFL4_YEAST	481	2.8	6	P43616	saccharomyc
296	1	PANF_ECOLI	483	2.8	6	P16256	escherichia
297	1	KPYK_CHLPN	484	2.8	6	Q9Z984	chlamydia p
298	1	PANF_HAEIN	484	2.8	6	P44963	haemophilus
299	1	PIGA_HUMAN	484	2.8	6	P37287	homo sapien
300	1	YG12_AQUAE	486	2.8	6	O67542	aquifex aeo
301	1	C72T_ARATH	490	2.8	6	Q9sae4	arabidopsis
302	1	HEMN_ALCEU	491	2.8	6	O34162	alcaligenes
303	1	NANT_ECOLI	496	2.8	6	P41036	escherichia
304	1	CPN2_MOUSE	500	2.8	6	P15539	mus musculus
305	1	ATPA_ACEWO	501	2.8	6	P50000	acetobacter
306	1	MYSU_RABIT	501	2.8	6	Q99105	oryctolagus
307	1	VATE_SCHPO	503	2.8	6	P31411	schizosacch
308	1	YS97_MYCTU	503	2.8	6	Q10818	mycobacteri
309	1	ATIN_HSVBP	504	2.8	6	P30020	bovine herp
310	1	IRF5_HUMAN	504	2.8	6	Q13568	homo sapien
311	1	SYK1_MYCTU	505	2.8	6	O06284	mycobacteri
312	1	GUX2_AGABI	506	2.8	6	Q92400	agaricus bi
313	1	GLPD_PSEAE	512	2.8	6	P52111	pseudomonas
314	1	HUTH_STRCO	512	2.8	6	Q9eww1	streptomyce
315	1	KAPB_SCHPO	512	2.8	6	P40376	schizosacch
316	1	NHAB_ECOLI	513	2.8	6	P27377	escherichia
317	1	HUTH_STRGR	514	2.8	6	P24221	streptomyce
318	1	NREA_SULDE	514	2.8	6	Q9Z4P4	sulfurospir
319	1	Y369_TREPA	516	2.8	6	O83384	treponema p
320	1	MMSA_CAEEL	523	2.8	6	P52713	caenorhabdi
321	1	NUON_MYCTU	531	2.8	6	O53308	mycobacteri
322	1	CP27_RABIT	535	2.8	6	P17177	o cytochrom
323	1	TLC2_CHLTR	541	2.8	6	O84502	chlamydia t
324	1	Y4MM_RHISN	541	2.8	6	P55572	rhizobium s
325	1	MKR3_MOUSE	544	2.8	6	Q60764	mus musculus

550	1	THDH_ARXAD	550	2.8	6	O42615	arxula aden
556	1	AGM1_ARATH	556	2.8	6	P57750	arabidopsis
556	1	PHL_LEPIN	556	2.8	6	P17627	leptospora
557	1	HLXB_SERMA	557	2.8	6	P15321	seriatia ma
557	1	MAOX_PIG	557	2.8	6	Q29558	sus scrofa
559	1	PHF1_MOUSE	559	2.8	6	Q921b8	mus musculus
562	1	YMX8_YEAST	562	2.8	6	O04301	saccharomyc
567	1	PHF1_HUMAN	567	2.8	6	O43189	homo sapien
576	1	T2BR_BACSU	576	2.8	6	P05529	bacillus su
589	1	RLD3_RAT	589	2.8	6	O88671	rattus norv
589	1	RRPO_BPOBE	589	2.8	6	P14647	bacterioph
591	1	PAK4_HUMAN	591	2.8	6	O96013	homo sapien
592	1	DLL3_MOUSE	592	2.8	6	O88516	mus musculus
596	1	NOLX_RHISN	596	2.8	6	P55711	rhizobium s
604	1	YJ16_YEAST	604	2.8	6	P47112	saccharomyc
607	1	PHEA_PSESP	607	2.8	6	P31020	pseudomonas
617	1	MUTA_PORGI	617	2.8	6	Q59676	porphyromon
617	1	SYP_SVNY3	617	2.8	6	P73942	synechocyst
618	1	T2D5_XENLA	618	2.8	6	Q91857	xenopus lae
620	1	AFR1_YEAST	620	2.8	6	P33304	saccharomyc
630	1	SOHC_ALIAC	630	2.8	6	P33247	allicyclobac
636	1	CAI3_RAT	636	2.8	6	P13941	rattus norv
637	1	P73_CERAE	637	2.8	6	Q9XSK8	cercopithec
643	1	DNAA_STRRE	643	2.8	6	Q9Zn76	streptomyce
655	1	ACDV_HUMAN	655	2.8	6	P49748	homo sapien
656	1	YC26_PORPU	656	2.8	6	P51392	porphyra pu
661	1	MX1_HUMAN	661	2.8	6	P20591	homo sapien
662	1	IL2R_HUMAN	662	2.8	6	P42701	homo sapien
666	1	YJB0_YEAST	666	2.8	6	P47077	saccharomyc
669	1	YH06_HAEIN	669	2.8	6	P45335	haemophilus
674	1	NUOL_NEIMA	674	2.8	6	Q9JX92	neisseria m
674	1	NUOL_NEIMB	674	2.8	6	Q9K1b0	neisseria m
683	1	BGH3_PIG	683	2.8	6	O11780	sus scrofa
690	1	VATI_DEIRA	690	2.8	6	Q9rwh3	deinococcus
692	1	PHLN_PSERE	692	2.8	6	P15713	pseudomonas
693	1	FSHR_CHICK	693	2.8	6	P79763	gallus gall
695	1	DIP2_MYCTU	695	2.8	6	Q10801	mycobacteri
702	1	TNSB_ECOLI	702	2.8	6	P13989	escherichia
704	1	GLGB_YEAST	704	2.8	6	P32775	saccharomyc
710	1	PMIP_RAT	710	2.8	6	Q01992	rattus norv
711	1	DCOR_ECOLI	711	2.8	6	P21169	escherichia
718	1	CTPC_MYCTU	718	2.8	6	P21169	escherichia
731	1	KCN3_MOUSE	731	2.8	6	P58391	mus musculus
732	1	DCOS_ECOLI	732	2.8	6	P24169	escherichia
732	1	KCN3_RAT	732	2.8	6	P70605	rattus norv
740	1	GAG_SMRVH	740	2.8	6	P21411	squirrel mo
774	1	STF_LAWBD	774	2.8	6	P03764	bacterioph
779	1	ACON_GRAVE	779	2.8	6	P49609	gracilaria
781	1	NANH_VIBCH	781	2.8	6	P37060	vibrio chol
784	1	DPO2_AERPE	784	2.8	6	Q93746	aeropyrum p
796	1	TRKA_HUMAN	796	2.8	6	P04629	homo sapien
799	1	TRKA_RAT	799	2.8	6	P35739	rattus norv
802	1	XPB_DROME	802	2.8	6	Q02870	drosophila
806	1	SUBV_BACSU	806	2.8	6	P29141	bacillus su
819	1	AK1H_SERMA	819	2.8	6	P27725	seriatia ma
825	1	QUTA_EMENI	825	2.8	6	P10563	emeritella
830	1	DYNI_CAEEL	830	2.8	6	P39055	caenorhabdi
831	1	NAPA_ALCEU	831	2.8	6	P39185	alcaligenes
831	1	NAPA_PARDT	831	2.8	6	Q56350	paracoccus
833	1	DL_DROME	833	2.8	6	P10041	drosophila
833	1	PTIA_ECOLI	833	2.8	6	P32670	escherichia
834	1	MSH5_HUMAN	834	2.8	6	O43196	homo sapien
836	1	GCSI_HUMAN	836	2.8	6	Q13724	homo sapien
836	1	PDC2_CANAL	836	2.8	6	O60035	candida alb
839	1	PHLD_BOVIN	839	2.8	6	P80109	bos taurus
854	1	KDPD_RATRA	854	2.8	6	O34971	rathayibact
855	1	NOLI_HUMAN	855	2.8	6	P46087	homo sapien
863	1	DPP6_BOVIN	863	2.8	6	P42659	bos taurus
865	1	DPP6_HUMAN	865	2.8	6	P42658	homo sapien
882	1	ALKS_PSEOL	882	2.8	6	P17051	pseudomonas
889	1	NODV_BRAJA	889	2.8	6	P15939	bradyrhizob
892	1	ATX7_HUMAN	892	2.8	6	O15265	homo sapien

399	1	ATMA_ECOLI	898	2.8	6	P39168	escherichia	472	6	2.8	4393	1	PGBM_HUMAN	P98160	homo sapien
400	1	ATMA_SALTY	902	2.8	6	P36640	salmonella	473	6	2.8	5217	1	HTSI_COCCA	Q01886	cochliobolu
401	1	DM3A_MOUSE	908	2.8	6	O88508	mus musculus	474	6	2.4	32	1	YTK3_ILTVT	P23985	infectiolus
402	1	DP01_BORBU	908	2.8	6	O51498	borrelia bu	475	5	2.4	33	1	YC12_CHLRE	P50370	chlamydomon
403	1	DM3A_HUMAN	912	2.8	6	O9y6k1	homo sapien	476	5	2.4	44	1	YCX9_ODOSI	P49835	odontella s
404	1	DNL3_HUMAN	922	2.8	6	P49916	homo sapien	477	5	2.4	45	1	GLB2_GLYDI	P02217	glycera dib
405	1	VGLB_HSVBC	932	2.8	6	P12640	bovine herp	478	5	2.4	49	1	R332_TREPA	Q06798	bacillus su
406	1	PAC4_RAT	937	2.8	6	Q63415	rattus norv	479	5	2.4	51	1	RL34_TREPA	O83917	treponema p
407	1	LBPA_NEIMA	943	2.8	6	Q06379	neisseria m	480	5	2.4	56	1	UCRY_BOVIN	P07552	bos taurus
408	1	LBPA_NEIMA	944	2.8	6	O9jtk4	neisseria m	481	5	2.4	56	1	UCRY_HUMAN	O14957	homo sapien
409	1	IF41_YEAST	952	2.8	6	P39935	saccharomyc	482	5	2.4	62	1	YM32_MARPO	P38470	marchantia
410	1	YC07_YEAST	953	2.8	6	P25618	saccharomyc	483	5	2.4	63	1	RL44_AERPE	O9y600	aeropyrum p
411	1	LONM_CAEEL	971	2.8	6	O44952	caenorhabdi	484	5	2.4	64	1	PHYB_PHYBI	P81565	phyllomedus
412	1	RPN1_YEAST	993	2.8	6	P38764	saccharomyc	485	5	2.4	64	1	Y05K_BPT4	P39238	bacteriochia
413	1	GLNE_MYCTU	994	2.8	6	Q10379	mycobacteri	486	5	2.4	65	1	YJET_ECOLI	P39289	escherichia
414	1	EPAB_MOUSE	1004	2.8	6	O09127	mus musculus	487	5	2.4	66	1	RLXN_RANCA	P39084	rana catesb
415	1	EPAB_HUMAN	1005	2.8	6	P29322	homo sapien	488	5	2.4	67	1	SAS2_BACSU	P04832	bacillus su
416	1	CA13_BOVIN	1049	2.8	6	P04258	bos taurus	489	5	2.4	67	1	TATE_SALTY	P57050	salmonella
417	1	UBA1_WHEAT	1051	2.8	6	P20973	trititum ae	490	5	2.4	68	1	V07K_PWV	P20954	papaya mosa
418	1	UBA2_WHEAT	1051	2.8	6	P31251	trititum ae	491	5	2.4	69	1	SAS1_BACSU	P04831	bacillus su
419	1	GCSP_PEA	1057	2.8	6	P26969	pisum sativ	492	5	2.4	69	1	Y4LI_RHISN	P55549	rhizobium s
420	1	NUP1_YEAST	1076	2.8	6	P20676	saccharomyc	493	5	2.4	69	1	Y842_ARCFU	O29416	archaeoglob
421	1	T2D3_HUMAN	1083	2.8	6	O00268	homo sapien	494	5	2.4	70	1	KAD_STRSC	P43417	streptomyce
422	1	IMB3_YEAST	1089	2.8	6	P32337	saccharomyc	495	5	2.4	70	1	MTRE_METMA	P80654	methanosarc
423	1	KPCI_ASPNG	1096	2.8	6	Q00078	aspergillus	496	5	2.4	70	1	SASI_BACST	P06552	bacillus sc
424	1	CHS1_YEAST	1131	2.8	6	P08004	saccharomyc	497	5	2.4	70	1	YAI2_ECOLI	P46270	solanan tub
425	1	MYSB_ACACA	1147	2.8	6	P19706	acanthamoeb	498	5	2.4	72	1	UCRX_SOLTU	P81068	mus musculus
426	1	SMRK_XIPMA	1167	2.8	6	P13388	xiphophorus	499	5	2.4	74	1	IRX1_MOUSE	O50638	leptospira
427	1	SRS2_YEAST	1175	2.8	6	P12954	saccharomyc	500	5	2.4	74	1	YIDD_LEPIN	P48438	brassica ol
428	1	PIB2_HUMAN	1181	2.8	6	Q00722	homo sapien	501	5	2.4	76	1	GTH_BRAOL	P14309	holothuria
429	1	CHS4_WAGGR	1198	2.8	6	O13353	magnaporthe	502	5	2.4	78	1	PHI0_HOLTU	P42544	bacterioph
430	1	CA13_CHICK	1262	2.8	6	P12105	gallus gall	503	5	2.4	78	1	Y009_BPL2	O16517	homo sapien
431	1	NGCA_CHICK	1266	2.8	6	Q03696	gallus gall	504	5	2.4	81	1	NNAT_HUMAN	O61979	mus musculus
432	1	DYNA_NEUCR	1300	2.8	6	Q01397	neurospora	505	5	2.4	81	1	NNAT_MOUSE	O62649	rattus norv
433	1	YMD9_YEAST	1328	2.8	6	Q03434	saccharomyc	506	5	2.4	81	1	NNAT_RAT	P21121	vaccinia vi
434	1	YME4_YEAST	1328	2.8	6	Q04711	saccharomyc	507	5	2.4	82	1	YVCC_VACCC	P18100	human immu
435	1	YMT5_YEAST	1328	2.8	6	Q04214	saccharomyc	508	5	2.4	87	1	VPR_HV2BE	Q9c523	mycobacteri
436	1	YMO0_YEAST	1328	2.8	6	Q04670	saccharomyc	509	5	2.4	88	1	RL27_MYCLE	O9vhs2	drosophila
437	1	CA21_ONCMY	1356	2.8	6	O93484	oncorhynch	510	5	2.4	89	1	COXJ_DROME	P05861	serrattia ma
438	1	Z198_HUMAN	1377	2.8	6	Q9ubw7	homo sapien	511	5	2.4	89	1	DRPH_ROMMI	P09929	romalea mic
439	1	RRPO_P1AMV	1385	2.8	6	Q07518	plantago as	512	5	2.4	89	1	RPOK_AERPE	O9yjd9	aeropyrum p
440	1	GTFD_STRMU	1462	2.8	6	P49331	streptococc	513	5	2.4	90	1	AF10_HUMAN	Q13015	homo sapien
441	1	CA13_HUMAN	1466	2.8	6	P02461	homo sapien	514	5	2.4	90	1	AF10_MOUSE	P97783	mus musculus
442	1	PR3G_MOUSE	1506	2.8	6	O70167	mus musculus	515	5	2.4	90	1	DBH1_BACHD	Q9kda5	bacillus ha
443	1	YJ79_YEAST	1755	2.8	6	P47098	saccharomyc	516	5	2.4	90	1	DBHB_SERMA	P52681	serrattia ma
444	1	YJ29_YEAST	1755	2.8	6	P47100	saccharomyc	517	5	2.4	90	1	REV_HV1ZH	P05868	human immu
445	1	MOT1_YEAST	1867	2.8	6	P32333	saccharomyc	518	5	2.4	92	1	DBH1_BACSU	P08821	mesocricetu
446	1	PTPF_HUMAN	1897	2.8	6	P10586	homo sapien	519	5	2.4	92	1	IAPP_MESAU	P23442	mesocricetu
447	1	PTPD_HUMAN	1912	2.8	6	P23468	homo sapien	520	5	2.4	92	1	PR10_CAYPO	P20658	cavia porce
448	1	MYHA_BOVIN	1976	2.8	6	Q27991	bos taurus	521	5	2.4	93	1	LI0K_RAT	Q05310	rattus norv
449	1	MYHA_HUMAN	1976	2.8	6	P35580	homo sapien	522	5	2.4	93	1	N36B_SOYBN	Q02919	glycine max
450	1	MYHA_RAT	1976	2.8	6	Q9jlt0	rattus norv	523	5	2.4	93	1	Y073_METJA	O60379	methanococc
451	1	CIN5_RAT	2019	2.8	6	P15389	rattus norv	524	5	2.4	94	1	AFP_ASPGI	P17737	aspergillus
452	1	FSH_DROME	2038	2.8	6	P13709	drosophila	525	5	2.4	94	1	DEF5_HUMAN	Q01523	homo sapien
453	1	TESU_HSV7J	2059	2.8	6	P52362	human herpe	526	5	2.4	95	1	DAFT_TRYCR	Q26327	trypanosoma
454	1	RRPL_VSVJH	2109	2.8	6	P13615	vesicular s	527	5	2.4	95	1	NQOB_THETH	Q56226	thermus aqu
455	1	RRPL_VSVJO	2109	2.8	6	P16379	vesicular s	528	5	2.4	95	1	YBUC_ECOLI	P46119	escherichia
456	1	RRPL_VSVSJ	2109	2.8	6	P03523	vesicular s	529	5	2.4	95	1	YF03_CLOPE	Q46213	clostridium
457	1	RRPL_RABVS	2127	2.8	6	P16289	rabies viru	530	5	2.4	96	1	CTC1_ACILW	O33947	acinetobact
458	1	RRPL_RABVP	2142	2.8	6	P11213	rabies viru	531	5	2.4	96	1	APC3_MOUSE	P33622	mus musculus
459	1	CCAE_RABIT	2259	2.8	6	Q02343	oryctolagus	532	5	2.4	99	1	PLAS_CUCSA	P00253	cucumis sat
460	1	POUG_EMCV	2290	2.8	6	P03304	encephalomy	533	5	2.4	99	1	PYY_DICUA	O9PT99	dicentrarch
461	1	POUG_EMCVB	2292	2.8	6	P17593	encephalomy	534	5	2.4	99	1	YIAB_YEAST	P40554	saccharomyc
462	1	POUG_EMCVD	2292	2.8	6	P17594	encephalomy	535	5	2.4	99	1	YY07_MYCTU	O50718	mycobacteri
463	1	FAS_HUMAN	2304	2.8	6	P49327	homo sapien	536	5	2.4	100	1	CKGK_CONGE	P07231	conus geogr
464	1	POIG_BCMVN	3066	2.8	6	Q65399	b genome po	537	5	2.4	100	1	PINL_HUMAN	O15428	homo sapien
465	1	ERY3_SACER	3172	2.8	6	Q03133	saccharopol	538	5	2.4	100	1	YE94_MYCTU	P17175	mycobacteri
466	1	POUG_DEN4	3386	2.8	6	P09866	d genome po	539	5	2.4	101	1	YOG4_CABEL	P34613	caenorhabdi
467	1	POUG_LANVT	3414	2.8	6	P29837	l genome po	540	5	2.4	101	1	APC2_CANFA	P12278	canis famil
468	1	ERY2_SACER	3567	2.8	6	Q03132	saccharopol	541	5	2.4	101	1	CH10_HUMAN	O04984	homo sapien
469	1	YAMB_SCHPO	3655	2.8	6	Q10064	schizosacch	542	5	2.4	101	1	CH10_MOUSE	O64433	mus musculus
470	1	PGBM_MOUSE	3707	2.8	6	Q05793	mus musculus	543	5	2.4	101	1	CH10_RAT	P26772	rattus norv
471	1	PRKD_HUMAN	4128	2.8	6	P78527	homo sapien	544	5	2.4	101	1	ELAB_ECOLI	P52084	escherichia

691	5	2.4	130	1	MIA_BOVIN	Q28038	bos taurus	764	141	1	DTD_STRCO	Q9k4f6	streptomyc
692	5	2.4	130	1	MIA_MOUSE	O61865	mus musculus	765	141	1	GLBI_PHESE	P11740	pheretima s
693	5	2.4	130	1	MIA_RAT	O62946	rattus norv	766	141	1	HBA_PSIKR	P19831	psittacula s
694	5	2.4	130	1	OREX_CANFA	O9glf6	canis fami	767	141	1	HBA_SPHU	P10059	sphenodon p
695	5	2.4	130	1	OREX_MOUSE	O55241	mus musculus	768	141	1	PHCO_BPT4	P04538	bacterioph
696	5	2.4	130	1	OREX_RAT	O55232	rattus norv	769	141	1	YC59_LISIN	O928a6	listeria in
697	5	2.4	130	1	RS11_THEMA	O9x1i4	thermotoga	770	142	1	CDD_YEAST	Q06549	saccharomyc
698	5	2.4	130	1	Y77_BT7	P03796	bacterioph	771	142	1	CDD_MUSVI	P11280	m corticotr
699	5	2.4	130	1	YE65_AQUAE	O67445	aquifex ao	772	142	1	E1BS_ADE04	P36595	schizosacch
700	5	2.4	130	1	YG31_PYRHO	O59297	pyrococcus	773	142	1	RPB6_SCHPO	P24353	astasia lon
701	5	2.4	131	1	AGSR_MOUSE	P56473	mus musculus	774	143	1	RR8_ASTLO	P52665	enterobacte
702	5	2.4	131	1	AGSM_MOUSE	Q03288	mus musculus	775	143	1	MUCR_RHISN	P55363	rhizobium s
703	5	2.4	131	1	AGSM_YULVU	P79407	vulpes vulp	776	143	1	NUSA_SULAC	P11523	sulfolobus
704	5	2.4	131	1	C79A_LOCMI	P45586	locusta mig	777	143	1	RK2_SOVEN	P18663	glycine max
705	5	2.4	131	1	C79B_LOCMI	P45587	locusta mig	778	143	1	YDL1_CORDI	P33118	corynebacte
706	5	2.4	131	1	C007_LOCMI	P11733	locusta mig	779	143	1	YL66_MYCLE	O69561	mycobacteri
707	5	2.4	131	1	MIA_HUMAN	Q16674	homo sapien	780	143	1	YL66_MYCTU	O06211	mycobacteri
708	5	2.4	131	1	OREX_HUMAN	Q43612	homo sapien	781	143	1	AGH_ARMVU	Q9u8r2	armadillidi
709	5	2.4	131	1	OREX_PIG	O77668	sus scrofa	782	144	1	GLB3_LAMSP	P15469	lamellibrac
710	5	2.4	131	1	PRO1_SOYBN	O65809	glycine max	783	144	1	GLB3_LAMSP	P80592	riftia pach
711	5	2.4	131	1	PRO2_HALDO	O9xf41	malus domes	784	144	1	GLBB_RIEPA	Q22054	caenorhabdi
712	5	2.4	131	1	PRO2_SOYBN	O65810	glycine max	785	144	1	RS16_CABEL	P14131	mus musculus
713	5	2.4	131	1	PROF_ARAHY	O98c19	arachis hyp	786	144	1	RS16_MOUSE	O83645	treponema p
714	5	2.4	131	1	RS26_ARATH	P05763	arabidopsis	787	144	1	Y638_TREPA	O56629	aspergillus
715	5	2.4	131	1	RS9_HALMA	P05763	haloarcula	788	145	1	CYB_ASPEL	P56630	aspergillus
716	5	2.4	131	1	RS9_HALN1	Q9hqj2	halobacteri	789	145	1	CYB_ASPEL	P35076	bordetella
717	5	2.4	131	1	V092_POMPV	Q9j5c8	owlpox vir	790	145	1	FIMA_BORPE	Q38662	bacterioph
718	5	2.4	131	1	Y405_METJA	O57848	methanococc	791	145	1	NINB_BPP22	P17008	homo sapien
719	5	2.4	131	1	AGSR_HUMAN	C00253	homo sapien	792	145	1	RS16_HUMAN	P55686	rhizobium s
720	5	2.4	132	1	AGSM_HUMAN	P42127	homo sapien	793	145	1	Y4WH_RHISN	P41332	microcephal
721	5	2.4	132	1	C560_CVACA	P48935	cyanidium c	794	146	1	HBB_MICGA	Q9xj11	bacterioph
722	5	2.4	132	1	CHA2_BOMMO	P08825	bombyx mori	795	146	1	NINB_BPP21	P03765	bacterioph
723	5	2.4	132	1	SZ05_MOUSE	P50228	mus musculus	796	146	1	NINB_LAMBD	P37539	bacillus su
724	5	2.4	132	1	YBL2_STRCI	P33654	streptomyc	797	146	1	YAAR_BACSU	P02141	oncorhynch
725	5	2.4	132	1	YOHU_ECOLI	P33372	escherichia	798	147	1	HBB4_ONCMY	P02139	cyrpinus ca
726	5	2.4	132	1	AGWS_BOVIN	Q29414	bos taurus	799	147	1	HBB_CARAU	P02140	carassius a
727	5	2.4	133	1	BRX2_SHEEP	Q9n0m2	ovis aries	800	147	1	HBB_CYPCA	Q98t50	oncorhynch
728	5	2.4	133	1	CDD_MYCPI	P47718	mycoplasma	801	147	1	HBB_SALSA	Q01473	salmo salar
729	5	2.4	133	1	CDD_MYCPN	P75051	mycoplasma	802	147	1	HBB_ONCNE	P77153	escherichia
730	5	2.4	133	1	OUTS_ERWCH	Q01567	erwinia chr	803	147	1	WZB_ECOLI	Q97862	oryctolagus
731	5	2.4	133	1	PEMK_ECOLI	P13976	escherichia	804	148	1	CYTC_RABIT	Q9vq62	oryctolagus
732	5	2.4	133	1	YONC_CABEL	Q09527	caenorhabdi	805	148	1	NP2C_DROME	Q10464	tritricum ae
733	5	2.4	134	1	CENA_MOUSE	O35216	mus musculus	806	148	1	PUIB_WHEAT	P43972	haemophilus
734	5	2.4	134	1	OAPB_HAEIN	P44416	haemophilus	807	148	1	Y246_HAEIN	Q54325	streptomyc
735	5	2.4	134	1	PRO1_ORYSA	P15839	oryza sativ	808	149	1	DTD_STRGR	P02220	tylorthynch
736	5	2.4	134	1	PROF_APIGR	Q9xf37	apium grave	809	149	1	GLB4_TYDHE	P11335	spiroplasma
737	5	2.4	134	1	RL32_HUMAN	P02433	homo sapien	810	149	1	VG3_SPV4	P21863	pseudomonas
738	5	2.4	134	1	RL3P_MOUSE	P17932	mus musculus	811	150	1	FKBX_PSEPL	Q51467	pseudomonas
739	5	2.4	134	1	RR9_GUITH	P19459	guillardia	812	150	1	FLIO_PSEAE	P14015	brugia paha
740	5	2.4	134	1	YHFA_ECOLI	P24246	escherichia	813	150	1	RS13_BRUPA	Q9z729	chlamydia p
741	5	2.4	135	1	CYB_APUPAP	Q33629	apus apus (814	150	1	Y877_CHLEN	Q03729	chlamydia p
742	5	2.4	135	1	IL4_BOVIN	P30367	bos taurus	815	150	1	YMBW_YEAST	Q03579	saccharomyc
743	5	2.4	135	1	IL4_CAPHI	P79155	capra hircu	816	151	1	DKSA_ECOLI	P15596	agrobacteri
744	5	2.4	135	1	IL4_SHEEP	P30368	ovis aries	817	151	1	MUP8_MOUSE	P18274	escherichia
745	5	2.4	135	1	VG46_HAEIN	P44239	haemophilus	818	151	1	RL19_PYRAB	P04938	mus musculus
746	5	2.4	135	1	RPB6_CABEL	Q17684	caenorhabdi	819	151	1	FCFL_PIG	Q9v1v3	pyrococcus
747	5	2.4	137	1	SPMI_PIG	Q28920	sus scrofa	820	152	1	GLBP_CHITH	P20002	sus scrofa
748	5	2.4	137	1	URE2_STAXY	P42874	staphylococ	821	152	1	MYG_APTFO	P11582	chironomus
749	5	2.4	137	1	VASH_BPP4	P05462	bacterioph	822	152	1	RS11_SCHPO	P79013	schizosacch
750	5	2.4	137	1	ESMA_DROME	Q97178	drosophila	823	152	1	SSB_RICPR	Q9zcc2	rickettsia
751	5	2.4	138	1	RS11_MYCLE	Q9x7a0	mycobacteri	824	152	1	VEL_FPVL	P06455	avian papil
752	5	2.4	138	1	VLL_BPV6	P50807	bovine papi	825	152	1	Y12G_BPT4	P32276	bacterioph
753	5	2.4	138	1	Y087_HUMAN	Q14695	homo sapien	826	153	1	ATP6_PSEPU	P25761	pseudomonas
754	5	2.4	138	1	Y560_METJA	O57980	methanococc	827	153	1	FLAP_HORSE	P30353	equus caball
755	5	2.4	139	1	RS11_MYCBO	P45812	mycobacteri	828	153	1	MYG_AOTTR	P02151	aotus trivi
756	5	2.4	139	1	RS11_MYCTU	O06326	mycobacteri	829	153	1	MYG_BALAC	P02179	balaenopter
757	5	2.4	139	1	Z014_XENLA	P18740	xenopus lae	830	153	1	MYG_BALPH	P02192	bos taurus
758	5	2.4	140	1	CWPX_ARATH	P47925	arabidopsis	831	153	1	MYG_BOVIN	P02152	callithrix
759	5	2.4	140	1	CYB_ASPTPE	P56631	aspergillus	832	153	1	MYG_CALJA	P02158	canis famill
760	5	2.4	140	1	RL14_AERPE	Q9yf82	aeropyrum p	833	153	1	MYG_CANFA	P14396	castor fibre
761	5	2.4	140	1	Y236_MYCGE	P47478	mycoplasma	834	153	1	MYG_CASFI	P02153	cebus apell
762	5	2.4	140	1	YE66_MYCPN	P75317	mycoplasma	835	153	1	MYG_CBBAP		
763	5	2.4	140	1	YRN3_VIBPA	P46231	vibrio para	836	153	1			

837	1	153	1	MYG_CEREL	P02191	cervus elap	910	5	2.4	157	1	PRTC_HORSE	Q28380	equus cabal
838	1	153	1	MYG_CHICK	P02197	gallus gall	911	5	2.4	157	1	RS11_DUNTE	P42756	dunaliella
839	1	153	1	MYG_CTREGU	P20856	ctenodactyl	912	5	2.4	157	1	UL51_HCMVA	P16792	human cytom
840	1	153	1	MYG_DIDMA	P02193	delphis m	913	5	2.4	158	1	COAD_PASMU	Q9cld4	pasteurella
841	1	153	1	MYG_ELEMA	P02186	elephas max	914	5	2.4	158	1	LUXS_LACIA	Q9ciu0	lactococcus
842	1	153	1	MYG_ERIEU	P02156	erinaceus e	915	5	2.4	158	1	RS11_HUMAN	P04643	homo sapien
843	1	153	1	MYG_ESGGI	P02177	eschrichtiu	916	5	2.4	158	1	RS11_XENLA	P41115	homo sapien
844	1	153	1	MYG_GALCR	P02168	galago cras	917	5	2.4	158	1	YV03_UREPA	Q9pr82	ureaplasma
845	1	153	1	MYG_GLOME	P02174	glodicephal	918	5	2.4	158	1	YV02_HUMAN	Q99765	homo sapien
846	1	153	1	MYG_GORBE	P02147	gorilla gor	919	5	2.4	159	1	BFR_MYCAV	P43314	mycobacteri
847	1	153	1	MYG_HALGR	P02162	halichoerus	920	5	2.4	159	1	BFR_MYCLE	P43315	mycobacteri
848	1	153	1	MYG_HORSE	P02188	equus cabal	921	5	2.4	159	1	BFR_MYCTU	O8465	mycobacteri
849	1	153	1	MYG_HUMAN	P02144	homo sapien	922	5	2.4	159	1	COAD_ECOLI	P23875	eschrichia
850	1	153	1	MYG_HYLAG	P02146	hylobates a	923	5	2.4	159	1	FAB2_HELPJ	Q9zjl6	helicobacte
851	1	153	1	MYG_INIGE	P02181	infa geoffir	924	5	2.4	159	1	FAB2_HELPY	O25928	helicobacte
852	1	153	1	MYG_KOGSI	P02184	kogia simus	925	5	2.4	159	1	OLF8_CHICK	Q98913	gallus gall
853	1	153	1	MYG_KAGLA	P02154	lagotrich l	926	5	2.4	159	1	R11B_ARATH	P42733	arabidopsis
854	1	153	1	MYG_LAGLA	P04250	lagostomus	927	5	2.4	159	1	R11G_ARATH	O65569	arabidopsis
855	1	153	1	MYG_LEPMU	P02169	lepilemur m	928	5	2.4	159	1	RS11_MAIZE	P25460	zea mays (m
856	1	153	1	MYG_LOXAF	P02187	loxodonta a	929	5	2.4	159	1	RS11_SOYBN	P17093	glycine max
857	1	153	1	MYG_LUTLU	P11343	lutra lutra	930	5	2.4	159	1	YC09_RHILO	Q983b3	rhizobium l
858	1	153	1	MYG_LYCPI	P02159	lycaon pict	931	5	2.4	160	1	R11A_ARATH	P16181	arabidopsis
859	1	153	1	MYG_MACRU	P02194	macropus ru	932	5	2.4	160	1	RS7_METBU	O39631	methanococc
860	1	153	1	MYG_MEGNO	P02178	megaptera n	933	5	2.4	161	1	PRTC_MACMU	Q28506	macaca mula
861	1	153	1	MYG_MELME	P02157	meles meles	934	5	2.4	161	1	SIXA_ECOLI	P76502	eschrichia
862	1	153	1	MYG_MESCA	P02183	mesopiodon	935	5	2.4	161	1	YA48_SCHPO	Q99727	schizosacch
863	1	153	1	MYG_MOUSE	P04247	mus musculus	936	5	2.4	161	1	YD03_MYCTU	Q10619	mycobacteri
864	1	153	1	MYG_NYCCO	P02167	nycticebus	937	5	2.4	161	1	YLAL_BACSU	O07636	bacillus su
865	1	153	1	MYG_OCHPR	P02171	ochotona pr	938	5	2.4	162	1	BAR2_CHIPA	P08725	chironomus
866	1	153	1	MYG_ONDZP	P32428	ondatra zib	939	5	2.4	162	1	CAB2_BOVIN	Q9n149	bos taurus
867	1	153	1	MYG_ORCOR	P02173	orcinus orc	940	5	2.4	162	1	FGFM_MOUSE	Q9ess2	mus musculu
868	1	153	1	MYG_ORYAF	P02164	orycteropus	941	5	2.4	162	1	R107_HUMAN	P53816	homo sapien
869	1	153	1	MYG_PANTR	P02145	pan troglod	942	5	2.4	163	1	R1SB_CORAM	O24753	corynebacte
870	1	153	1	MYG_PERPO	P02166	perodicticu	943	5	2.4	163	1	RS10_DROME	Q9vbl4	drosophila
871	1	153	1	MYG_PHOPH	P02176	phocoenoid	944	5	2.4	163	1	US34_HCMVA	P09709	human cytom
872	1	153	1	MYG_PHOSI	P30562	phoca sibir	945	5	2.4	165	1	R1MM_RICPR	Q9zdl0	rickettia
873	1	153	1	MYG_PHYCA	P02185	physeter ca	946	5	2.4	165	1	RS10_XENLA	Q07254	xenopus lae
874	1	153	1	MYG_PIG	P02189	sus scrofa	947	5	2.4	165	1	YAHC_ECOLI	P77219	eschrichia
875	1	153	1	MYG_PONPY	P02148	pongo pygma	948	5	2.4	165	1	YG06_YEAST	P53095	saccharomyc
876	1	153	1	MYG_PROGU	P04249	proechimys	949	5	2.4	166	1	LUXS_HAEIN	P44007	haemophilus
877	1	153	1	MYG_RABIT	P02170	oryctolagus	950	5	2.4	166	1	NUOE_ECOLI	P33601	eschrichia
878	1	153	1	MYG_ROUAE	P02163	rousettus a	951	5	2.4	166	1	NUOE_SALTU	P33903	salmonella
879	1	153	1	MYG_SHEEP	P02190	ovis aries	952	5	2.4	166	1	PAL_PSEPU	P43036	pseudomonas
880	1	153	1	MYG_SPAEH	P04248	spalax leuc	953	5	2.4	166	1	RL14_DROME	P55841	ictalurus p
881	1	153	1	MYG_TACAC	P02195	tachyglossu	954	5	2.4	166	1	RS10_ICTPU	Q90yr4	actinurus p
882	1	153	1	MYG_TUPGL	P02165	tupaia glis	955	5	2.4	167	1	HPPK_BACSU	P29252	bacillus su
883	1	153	1	MYG_TURTR	P02172	tursiops tr	956	5	2.4	167	1	YBL3_FOAMV	P14355	human spuma
884	1	153	1	MYG_VULCH	P02160	vulpes cham	957	5	2.4	167	1	YHBS_ECOLI	P04573	eschrichia
885	1	153	1	MYG_ZALCA	P02161	zalophus ca	958	5	2.4	167	1	YMW1_YEAST	Q04767	saccharomyc
886	1	153	1	MYG_ZIPCA	P02182	ziphius cav	959	5	2.4	168	1	LUXS_PASMU	P37901	pasteurella
887	1	154	1	FMK1_PSEAE	P17836	pseudomonas	960	5	2.4	168	1	TRIC_CHICK	Q10344	schizosacch
888	1	154	1	INLA_DROME	O9v50	drosophila	961	5	2.4	168	1	VTU2_DROME	P27673	gallus gall
889	1	154	1	MYG_ALLMI	P02200	alligator m	962	5	2.4	168	1	YB26_METJA	P13238	drosophila
890	1	155	1	FGF1_BOVIN	P03968	bos taurus	963	5	2.4	169	1	ACPS_THESA	Q58821	methanococc
891	1	155	1	FGF1_CHICK	P19596	gallus gall	964	5	2.4	169	1	CAFI_DICDI	O9vzf6	thermotoga
892	1	155	1	FGF1_HUMAN	P05230	homo sapien	965	5	2.4	169	1	FRBS_BOVIN	P54670	dictyosceli
893	1	155	1	FGF1_MESAU	P34004	mesocricetu	966	5	2.4	169	1	END4_METTH	P30535	bos taurus
894	1	155	1	FGF1_MOUSE	P10935	mus musculus	967	5	2.4	169	1	RGSD_CAEEL	P49808	caenorhabdi
895	1	155	1	LIPB_PARVE	Q00520	paracoccus	968	5	2.4	170	1	ENDA_METTH	O07165	methanobact
896	1	155	1	PCP_YEREN	P31484	yersinia en	969	5	2.4	170	1	FGFM_HUMAN	P09ct0	homo sapien
897	1	155	1	RL21_PYUST	P49667	pyura stolo	970	5	2.4	170	1	LUXS_ECOLI	P45578	eschrichia
898	1	155	1	SLYB_ECOLI	P20435	saccharomyc	971	5	2.4	170	1	LUXS_SALTU	Q914t0	salmonella
899	1	155	1	SLYB_SALTU	P55741	eschrichia	972	5	2.4	170	1	MSRA_SCHPO	Q09859	schizosacch
900	1	155	1	YF45_PSEAE	Q04628	pseudomonas	973	5	2.4	170	1	Y97X_HAEIN	O86230	haemophilus
901	1	156	1	LSPA_BACHD	Q9K9v2	bacillus ha	974	5	2.4	171	1	ARGR_CORGL	O85175	corynebacte
902	1	156	1	YMS6_CAEEL	P34502	caenorhabdi	975	5	2.4	171	1	FMS1_ECOLI	P25730	eschrichia
903	1	156	1	YMS6_MYCTU	O05808	mycobacteri	976	5	2.4	171	1	LUXS_VIBHA	Q9z5x1	vibrio harv
904	1	157	1	HME_CHICK	Q91975	gallus gall	977	5	2.4	171	1	RL10_LACLA	Q9c941	lactococcus
905	1	157	1	LUXS_BOVIN	O50164	borrelia bu	978	5	2.4	171	1	YCX7_YEAST	P25652	saccharomyc
906	1	157	1	ML14_BRARE	Q90456	brachydanio	979	5	2.4	171	1	YSNB_BACSU	P94559	bacillus su
907	1	157	1	PRTC_CANFA	Q28278	canis famil	980	5	2.4	172	1	GLNA_BOVIN	P15103	bos taurus
908	1	157	1	PRTC_CAPHI	Q28315	capra hircu	981	5	2.4	172	1	IM7B_HUMAN	O60830	homo sapien
909	1	157	1				982	5	2.4	172	1	PHB1_FREDI	P07119	fremyella d

983 5 2.4 172 1 PHB1_PSEA9 Q52446 pseudanabae
 984 5 2.4 172 1 PHB2_PSEA9 Q52451 pseudanabae
 985 5 2.4 172 1 PHCB_GALSU P00311 galdieria s
 986 5 2.4 172 1 PHCB_MASUA P00310 mastigoclad
 987 5 2.4 172 1 PHCB_SPIPL P72508 spirulina p
 988 5 2.4 172 1 PHCB_SYNY1 P20777 synechocyst
 989 5 2.4 172 1 RL10_CAUCR P58060 caulobacter
 990 5 2.4 172 1 YD52_SCHPO Q10307 schizosacch
 991 5 2.4 173 1 APRL_DROME Q8x263 drosophila
 992 5 2.4 173 1 CAB5_HUMAN Q9np86 homo sapien
 993 5 2.4 173 1 COBP_PSEDE P29931 pseudomonas
 994 5 2.4 173 1 PAL_ECOLI P07176 escherichia
 995 5 2.4 173 1 PHCB_FREDI P14877 fremyella d
 996 5 2.4 173 1 PHCB_ANASP P07120 anabaena sp
 997 5 2.4 173 1 YA92_MYCPN P75600 mycoplasma
 998 5 2.4 174 1 RECX_MYCTU Q33280 mycobacteri
 999 5 2.4 174 1 RU5_HALNI P50558 halobacteri
 1000 5 2.4 174 1 VGAM_BPMU P06023 bacteriophag

ALIGNMENTS

RESULT 1
 FGFK_HUMAN STANDARD; PRT; 211 AA.
 AC Q9NP95;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fibroblast growth factor-20 (FGF-20).
 GN FGF20.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20374469; PubMed=10913340;
 RA Kirikoshi H., Sagara N., Saitoh T., Tanaka K., Sekihara H.,
 RA Shiokawa K., Katoh M.;
 RT "Molecular cloning and characterization of human FGF-20 on chromosome
 RT 8p21.3-p22.2";
 RL Biochem. Biophys. Res. Commun. 274:337-343(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Itoh N.;
 RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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 CC
 CC EMBL; AB044277; BAB03633.1; -;
 CC EMBL; AB030648; BAB03530.1; -;
 CC MIM; 605558; -;
 CC InterPro; IPR002209; HBGFG_FGF.
 CC InterPro; IPR002348; ILL_HBGF.
 CC Pfam; PF00167; FGF; 1.
 CC PRINTS; PR00262; ILLHBGF.
 CC ProDom; PD000831; HBGFG_FGF; 1.
 CC SMART; SM00442; FGF; 1.
 CC PROSITE; PS00247; HBGFG_FGF; 1.
 KW Growth factor.
 SQ SEQUENCE 211 AA; 23498 MW; AB04608C16060CC1 CRC64;

Query Match 100.0%; Score 211; DB 1; Length 211;

Best Local Similarity 100.0%; Pred. No. 2.6e-211;
 Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPLAEEVGGELGGLGQGVGSHFLPPAGRPPLLGERRSAAERSARGGPGAAOLAHLL 60
 DB 1 MAPLAEEVGGELGGLGQGVGSHFLPPAGRPPLLGERRSAAERSARGGPGAAOLAHLL 60
 QY 61 HGILRRRLQYCRTFHQLIIPDGSVQCTQDHSILFGILEFISVAVGLSVIRGVDGSLYL 120
 DB 61 HGILRRRLQYCRTFHQLIIPDGSVQCTQDHSILFGILEFISVAVGLSVIRGVDGSLYL 120
 QY 121 MNDKGLYSGSKLTSECIFRQPEENWYNNYSNIYKHGTGRYFVALNKGDTPRDGR 180
 DB 121 MNDKGLYSGSKLTSECIFRQPEENWYNNYSNIYKHGTGRYFVALNKGDTPRDGR 180
 QY 181 SKRHQKTHFLPRVDPERPVELYKOLLMT 211
 DB 181 SKRHQKTHFLPRVDPERPVELYKOLLMT 211
 RESULT 2
 FGF9_XENLA STANDARD; PRT; 209 AA.
 AC Q91875;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE GliA-activating factor precursor (GAF) (Fibroblast growth factor-9)
 DE (FGF-9) (HBGF-9) (XFGF-9).
 GN FGF9.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97006698; PubMed=8853991;
 RA Song J., Slack J.M.W.;
 RT "XFGF-9: a new fibroblast growth factor from Xenopus embryos";
 RL Dev. Dyn. 206:427-436(1996).
 CC -!- FUNCTION: MAY HAVE A ROLE IN MUSCLE DEVELOPMENT AND NEURAL
 CC DIFFERENTIATION. HAS NO SPECIFIC ROLE IN ANTEROPOSTERIOR
 CC PATTERNING.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: MATERNAL TRANSCRIPT IS FOUND MAINLY IN THE
 CC ANIMAL HEMISPHERE. ZYGOTIC TRANSCRIPT IS FOUND AROUND THE
 CC BLASTOPORE AND IN THE LATE GASTRULA STAGE, IN THE DORSAL PART. IN
 CC LATER STAGES IT IS FOUND ALONG THE DORSAL PART AND HEAD REGION.
 CC -!- DEVELOPMENTAL STAGE: THE MATERNAL PROTEIN IS DETECTED UP TO THE
 CC BLASTULA STAGE BUT DECLINES BY THE EARLY GASTRULA. ZYGOTIC
 CC EXPRESSION STARTS AT AROUND EARLY GASTRULA; THE LEVEL OF
 CC EXPRESSION REACHED AT STAGE 15 PERSISTS DURING NEURULA AND TAILBUD
 CC STAGES, AND IS FURTHER INCREASED DURING THE TADPOLE STAGES.
 CC -!- PTM: KNOWN TO BE GLYCOSYLATED.
 CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
 CC
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 CC
 CC EMBL; U47622; AAC59936.1; -;
 CC HSSP; P05230; 2AFG
 CC InterPro; IPR002209; HBGFG_FGF.
 CC InterPro; IPR002348; ILL_HBGF.
 CC Pfam; PF00167; FGF; 1.
 CC PRINTS; PR00262; ILLHBGF.
 CC ProDom; PD000831; HBGFG_FGF; 1.
 CC SMART; SM00442; FGF; 1.


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DR PROSITE; PS00247; HBGF_FGF; 1.
KW Growth factor; Differentiation; Mitogen; Heparin-binding;
FT PROPEP 1 3 BY SIMILARITY.
FT CHAIN 4 209 GLIA-ACTIVATING FACTOR.
FT CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 209 AA; 23662 MW; 26CBB22977FCBFB CRC64;

Query Match 9.5%; Score 20; DB 1; Length 209;
Best Local Similarity 100.0%; Pred. No. 4c-13; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 139 FREQFEENWNTYSSNIYKH 158
      |||||
Db 137 FREQFEENWNTYSSNIYKH 156

RESULT 3
ID FGF9_HUMAN STANDARD; PRT; 208 AA.
AC P31371;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glia-activating factor precursor (GAF) (Fibroblast growth factor-9)
DE (FGF-9) (HBGF-9).
GN FGF9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Forebrain;
RX MEDLINE=93309459; PubMed=8321227;
RA Miyamoto M., Naruo K.-I., Seko C., Matsumoto S., Kondo T.,
RA Kurokawa T.;
RT "Molecular cloning of a novel cytokine cDNA encoding the ninth member
RT of the fibroblast growth factor family, which has a unique secretion
RT property.";
RL Mol. Cell. Biol. 13:4251-4259(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Blakey S.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 4-26 AND 34-54.
RC TISSUE=Glial tumor;
RX MEDLINE=93155105; PubMed=8428960;
RA Naruo K.-I., Seko C., Kuroshima K.-I., Matsutani E., Sasada R.,
RA Kondo T., Kurokawa T.;
RT "Novel secretory heparin-binding factors from human glioma cells
RT (glia-activating factors) involved in glial cell growth.
RT Purification and biological properties.";
RL J. Biol. Chem. 268:2857-2864(1993).
RN [4]
RX X-RAY CRYSTALLOGRAPHY (2.60 ANGSTROMS).
RP MEDLINE=21127675; PubMed=11223514;
RA Hecht H.J., Adar R., Hofmann B., Bogin O., Weich H., Yayon A.;
RT "Structure of fibroblast growth factor 9 shows a symmetric dimer with
RT unique receptor- and heparin-binding interfaces.";
RL Acta Crystallogr. D 57:378-384(2001).
CC -1- FUNCTION: MAY HAVE A ROLE IN GLIAL CELL GROWTH AND DIFFERENTIATION
CC DURING DEVELOPMENT, GLIOSIS DURING REPAIR AND REGENERATION OF
CC BRAIN TISSUE AFTER DAMAGE, DIFFERENTIATION AND SURVIVAL OF
CC NEURONAL CELLS, AND GROWTH STIMULATION OF GLIAL TUMORS.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: GLIAL CELLS.
CC -1- PTM: THREE MOLECULAR SPECIES WERE FOUND (30 KDA, 29 KDA AND 25
CC KDA), CLEAVED AT LEU-4, VAL-13 AND SER-34 RESPECTIVELY. THE
CC SMALLER ONES MIGHT BE PRODUCTS OF PROTEOLYTIC DIGESTION.
CC FURTHERMORE, THERE MAY BE A FUNCTIONAL SIGNAL SEQUENCE IN THE 30
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RT during induction of neuronal differentiation of mouse embryonal
RL carcinoma P19 cells."
RL FEBS Lett. 370:231-235(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96192599; PubMed=8619928;
RA Hecht D., Zimmerman N., Bedford M., Avivi A., Yayon A.;
RT "Identification of fibroblast growth factor 9 (FGF9) as a high
RT affinity, heparin dependent ligand for FGF receptors 3 and 2 but not
RT for FGF receptors 1 and 4."
RL Growth Factors 12:223-233(1995).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Colvin J.S., Feldman B., Nadeau J.H., Goldfarb M., Ornitz D.M.;
RT "Genomic organization and embryonic expression of the mouse fibroblast
RT growth factor 9 gene."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY HAVE A ROLE IN GLIAL CELL GROWTH AND DIFFERENTIATION
CC DURING DEVELOPMENT, GLIOSIS DURING REPAIR AND REGENERATION OF
CC BRAIN TISSUE AFTER DAMAGE, DIFFERENTIATION AND SURVIVAL OF
CC NEURONAL CELLS, AND GROWTH STIMULATION OF GLIAL TUMORS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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CC
CC EMBL; U33535; AAC52529.1; -
CC DR EMBL; D38258; BAA07410.1; -
CC DR EMBL; S82023; AAB36429.1; -
CC DR EMBL; AF144626; AAD49222.1; -
CC DR EMBL; AF144624; AAD49222.1; JOINED.
CC DR EMBL; AF144625; AAD49222.1; JOINED.
CC DR HSSP; P05230; 2AFG.
CC DR MGD; MGI:104723; Fgfg.
CC DR InterPro; IPR002209; HBGF_FGF.
CC DR InterPro; IPR002348; ILL_HBGF.
CC DR Pfam; PF00167; FGF; 1.
CC DR PRINTS; P000262; ILIHBGF.
CC DR ProDom; PD000831; HBGF_FGF; 1.
CC DR SMART; SM00442; FGF; 1.
CC DR PROSITE; PS00247; HBGF_FGF; 1.
CC KW Growth factor; Differentiation; Mitogen; Heparin-binding;
CC KW Glycoprotein.
CC FT PROPEP 1 3 BY SIMILARITY.
CC FT CHAIN 4 208 GLIA-ACTIVATING FACTOR.
CC FT CARBOHYD 79 79 N-LINKED (GLCNAC...) (POTENTIAL).
CC SQ SEQUENCE 208 AA; 23440 MW; E8DE1EDFE70979E CRC64;

Query Match 9.0%; Score 19; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 4.3e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLSVIRGVDGSLYLGMN 122
Db 101 AVGLSVIRGVDGSLYLGMN 119

RESULT 5
FGF9_RAT
ID FGF9_RAT STANDARD; PRT; 208 AA.
AC F36364;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Glia-activating factor precursor (GAF) (Fibroblast growth factor-9)
DE (FGF-9) (HBGF-9).

Query Match 9.0%; Score 19; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 4.3e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLSVIRGVDGSLYLGMN 122
Db 101 AVGLSVIRGVDGSLYLGMN 119

RESULT 6
FGFG_HUMAN
ID FGFG_HUMAN STANDARD; PRT; 207 AA.
AC O43320;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fibroblast growth factor-16 (FGF-16).
GN FGF16.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;

GN FGF9 OR FGF-9.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93309459; PubMed=8321227;
RA Miyamoto M., Naruo K.-I., Seko C., Matsumoto S., Kondo T.,
RA Kurokawa T.;
RT "Molecular cloning of a novel cytokine cDNA encoding the ninth member
RT of the fibroblast growth factor family, which has a unique secretion
RT property."
RL Mol. Cell. Biol. 13:4251-4259(1993).
CC -!- FUNCTION: MAY HAVE A ROLE IN GLIAL CELL GROWTH AND DIFFERENTIATION
CC DURING DEVELOPMENT, GLIOSIS DURING REPAIR AND REGENERATION OF
CC BRAIN TISSUE AFTER DAMAGE, DIFFERENTIATION AND SURVIVAL OF
CC NEURONAL CELLS, AND GROWTH STIMULATION OF GLIAL TUMORS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: BRAIN AND KIDNEY.
CC -!- PTM: N-GLYCOSYLATED.
CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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CC
CC EMBL; D14839; BAA03573.1; -
CC DR HSSP; P05230; 2AFG.
CC DR InterPro; IPR002209; HBGF_FGF.
CC DR InterPro; IPR002348; ILL_HBGF.
CC DR Pfam; PF00167; FGF; 1.
CC DR PRINTS; P000262; ILIHBGF.
CC DR ProDom; PD000831; HBGF_FGF; 1.
CC DR SMART; SM00442; FGF; 1.
CC DR PROSITE; PS00247; HBGF_FGF; 1.
CC KW Growth factor; Differentiation; Mitogen; Heparin-binding;
CC KW Glycoprotein.
CC FT PROPEP 1 3 BY SIMILARITY.
CC FT CHAIN 4 208 GLIA-ACTIVATING FACTOR.
CC FT CARBOHYD 79 79 N-LINKED (GLCNAC...) (POTENTIAL).
CC SQ SEQUENCE 208 AA; 23413 MW; 4A3CE894DF643EB CRC64;

Query Match 9.0%; Score 19; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 4.3e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLSVIRGVDGSLYLGMN 122
Db 101 AVGLSVIRGVDGSLYLGMN 119

RESULT 6
FGFG_HUMAN
ID FGFG_HUMAN STANDARD; PRT; 207 AA.
AC O43320;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fibroblast growth factor-16 (FGF-16).
GN FGF16.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;

```

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RX MEDLINE=98139883; PubMed=9473496;
RA Miyake A., Konishi M., Martin F.H., Hernday N.A., Ozaki K.,
RA Yamamoto S., Mikami T., Arakawa T., Itoh N.;
RT "Structure and expression of a novel member, FGF-16, on the fibroblast
RT growth factor family.";
RL Biochem. Biophys. Res. Commun. 243:148-152(1998).
CC -1- FUNCTION: INDUCES HEPATOCELLULAR PROLIFERATION. HAS NO BIOLOGICAL
CC EFFECT ON THE HEART (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC -----
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CC -----
CC EMBL; AB009391; BAA24956.1; -.
CC HSSP; P05230; 2AFG.
CC MIM; 603724; -.
CC InterPro; IPR002209; HBGF_FGF.
CC InterPro; IPR002348; ILI_HBGF.
CC Pfam; PF00167; FGF; 1.
CC PRINTS; PR00262; ILIHBGF.
CC ProDom; PD000831; HBGF_FGF; 1.
CC SMART; SM00442; FGF; 1.
CC SMART; SM00442; FGF; 1.
CC PROSITE; PS00247; HBGF_FGF; 1.
CC Growth factor.
CC CARBOHYD 78 78 N-LINKED (GLCNAC... ) (POTENTIAL).
FT SEQUENCE 207 AA; 23759 MW; D8AD160DABDB5F8 CRC64;
SQ

Query Match 7.6%; Score 16; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 5.6e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 GILRRRLQYCRGTGFHL 77
Db 58 GILRRRLQYCRGTGFHL 73

RESULT 7
FGFG_RAT ID FGFG_RAT STANDARD; PRT; 207 AA.
AC OS4769;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fibroblast growth factor-16 (FGF-16).
GN FGF16.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR;
RX MEDLINE=98139883; PubMed=9473496;
RA Miyake A., Konishi M., Martin F.H., Hernday N.A., Ozaki K.,
RA Yamamoto S., Mikami T., Arakawa T., Itoh N.;
RT "Structure and expression of a novel member, FGF-16, on the fibroblast
RT growth factor family.";
RL Biochem. Biophys. Res. Commun. 243:148-152(1998).
CC -1- FUNCTION: INDUCES HEPATOCELLULAR PROLIFERATION. HAS NO BIOLOGICAL
CC EFFECT ON THE HEART. MAY PLAY A ROLE IN THE DEVELOPMENT OF
CC EMBRYONIC BROWN ADIPOSE TISSUE.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: IN ADULT, PREDOMINANTLY EXPRESSED IN HEART, IN
CC THE CARDIAC MYOCYTES. NOT DETECTED IN BRAIN, LUNG, LIVER, KIDNEY
CC AND WHITE ADIPOSE TISSUE. IN EMBRYOS, PREDOMINANTLY EXPRESSED IN
CC THE BROWN ADIPOSE TISSUE.
CC -1- DEVELOPMENTAL STAGE: EXPRESSION IN BROWN ADIPOSE TISSUE DECREASED

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CC GREATLY AFTER BIRTH.
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC -----
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CC -----
CC EMBL; AB002561; BAA24947.1; -.
CC HSSP; P09038; 1BFG.
CC InterPro; IPR002209; HBGF_FGF.
CC InterPro; IPR002348; ILI_HBGF.
CC Pfam; PF00167; FGF; 1.
CC PRINTS; PR00262; ILIHBGF.
CC ProDom; PD000831; HBGF_FGF; 1.
CC SMART; SM00442; FGF; 1.
CC PROSITE; PS00247; HBGF_FGF; 1.
CC Growth factor.
CC CARBOHYD 78 78 N-LINKED (GLCNAC... ) (POTENTIAL).
FT SEQUENCE 207 AA; 23753 MW; IC7A11C8BA3164BC CRC64;
SQ

Query Match 7.6%; Score 16; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 5.6e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 GILRRRLQYCRGTGFHL 77
Db 58 GILRRRLQYCRGTGFHL 73

RESULT 8
Y273_METH ID Y273_METH STANDARD; PRT; 151 AA.
AC O26373;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MTH273.
GN MTH273.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanothermobacter.
OX NCBI_TaxID=145262;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DELTA H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
CC -1- SIMILARITY: BELONGS TO THE UPF0098 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE000813; AAB84779.1; -.
CC Hypothetical protein; Complete proteome.
KW SEQUENCE 151 AA; 16497 MW; 575075BBBC70464E0 CRC64;
SQ

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Query Match          3.8%; Score 8; DB 1; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 LPDGSVQG 87
DB 80 LPDGSVQG 87

RESULT 9
YD58_CAUCR
ID YD58_CAUCR STANDARD; PRT; 157 AA.
AC Q9A8J5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein CCI1358.
GN CCI1358.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=69394;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 19089 / CB15;
RC MEDLINE=21173698; PubMed=11259647;
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC -!- SIMILARITY: BELONGS TO THE UPF0168 FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AE005811; AAK23339.1; -
DR TIGR; CC1358; -
DR InterPro; IPR003796; DUF193.
DR Pfam; PF02644; DUF193; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 157 AA; 17854 MW; 0F1F23C17784614C CRC64;

Query Match          3.8%; Score 8; DB 1; Length 157;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 RPVDPERV 200
DB 77 RPVDPERV 84

RESULT 10
Y665_HUMAN
ID Y665_HUMAN STANDARD; PRT; 756 AA.
AC Q75154; Q9NU10; Q9H1G0; Q9H155;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein KIAA0665.
GN KIAA0665.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98403880; PubMed=9734811;
RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
RA Kotani H., Nomura N., Ohara O.;
RA "Prediction of the coding sequences of unidentified human genes. X.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:169-176(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21096910; PubMed=11157797;
RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA Higgs D.R.;
RT "Sequence, structure and pathology of the fully annotated terminal 2
RT Mb of the short arm of human chromosome 16.";
RL Hum. Mol. Genet. 10:339-352(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Wallis J., Lloyd C., Hall R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC
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CC
CC EMBL; AB014565; BAA31640.1; -
DR EMBL; AE006463; AAK61232.1; -
DR EMBL; AL023881; CAB92745.1; -
DR EMBL; AL049542; CAC17519.1; -
DR EMBL; Z98882; CAC17523.1; -
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 2
KW Hypothetical protein; Calcium-binding; Repeat.
FT CA_BIND 215 226 EF-HAND 1 (POTENTIAL).
FT CA_BIND 247 258 EF-HAND 2 (POTENTIAL).
SQ SEQUENCE 756 AA; 82439 MW; 264CEC399F28AFB9 CRC64;

Query Match          3.8%; Score 8; DB 1; Length 756;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GPGAAQLA 58
DB 26 GPGAAQLA 33

RESULT 11
AT2A_HUMAN
ID AT2A_HUMAN STANDARD; PRT; 1047 AA.
AC Q75110; Q9NQK6; Q9NQK7;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Potential phospholipid-transporting ATPase IIA (EC 3.6.1.-).
GN ATP9A OR KIAA0611.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 15-1047 FROM N.A. (SHORT ISOFORM).
RC TISSUE=Brain;
RX MEDLINE=98403880; PubMed=9734811;

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RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
 RA Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. X.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:169-176(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhani P., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Houlden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Levaslaiho M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
 RA Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 CC -!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + PHOSPHATE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING
 CC -!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
 CC ATPASES). SUBFAMILY IV.
 CC -----
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 CC -----
 DR EMBL; AB014511; BAA31586.1; -
 DR EMBL; AL335799; CAC17554.1; -
 DR EMBL; AL138807; CAB92773.1; -
 DR EMBL; AL035684; CAB63450.1; -
 DR EMBL; AL138807; CAB92774.1; ALT_SEQ.
 DR InterPro: IPR001757; E1-E2_ATPase.
 DR Pfam: PF00702; Hydrolase; 1.
 DR PROSITE: PR00119; CATATPASE
 DR PROSITE: PS00154; ATPASE_E1E2; 1.
 KW Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
 KW Alternative splicing; Multigene family.
 FT DOMAIN 1 69
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 70 91
 FT POTENTIAL.
 FT DOMAIN 92 96
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 97 119
 FT POTENTIAL.
 FT DOMAIN 120 303
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 304 325
 FT POTENTIAL.
 FT DOMAIN 326 332
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 333 354
 FT POTENTIAL.
 FT DOMAIN 355 841
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 842 862
 FT POTENTIAL.
 FT DOMAIN 863 874
 FT EXTRACELLULAR (POTENTIAL).
 FT

FT TRANSMEM 875 893 POTENTIAL.
 FT DOMAIN 894 923 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 924 942 POTENTIAL.
 FT DOMAIN 943 949 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 950 972 POTENTIAL.
 FT DOMAIN 973 978 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 979 999 POTENTIAL.
 FT DOMAIN 1000 1006 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1007 1030 POTENTIAL.
 FT DOMAIN 1031 1047 CYTOPLASMIC (POTENTIAL).
 FT MOD_RES 391 391 PHOSPHORYLATION (BY SIMILARITY).
 FT METAL 785 785 MAGNESIUM (BY SIMILARITY).
 FT METAL 789 789 MAGNESIUM (BY SIMILARITY).
 FT VARSPLIC 149 269 MISSING (IN SHORT ISOFORM).
 SQ SEQUENCE 1047 AA; 118582 MW; 80C307CF5A396755 CRC64;
 Query Match 3.8%; Score 8; DB 1; Length 1047;
 Best Local Similarity 100.0%; Pred. No. 4.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 201 PELYKDLL 208
 Db 907 PELYKDLL 914
 RESULT 12
 AT9A_MOUSE
 ID AT9A_MOUSE STANDARD; PRT; 1047 AA.
 AC 070228;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotating update)
 DE Potential phospholipid-transporting ATPase IIA (EC 3.6.3.1).
 GN ATP9A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20473714; PubMed=11015572;
 RA Halleck M.S., Lawler J.F. Jr., Blackshaw S., Gao L., Nagarajan P.,
 RA Hacker C., Pyle S., Newman J.T., Nakanishi Y., Ando H., Weinstock D.,
 RA Williamson P., Schlegel R.A.;
 RT "Differential expression of putative transbilayer amphipath
 RT transporters.";
 RL Physiol. Genomics 1:139-150(1999).
 RN [2]
 RP SEQUENCE OF 28-1047 FROM N.A.
 RX MEDLINE=98217376; PubMed=9548971;
 RA Halleck M.S., Pradhan D., Blackman C.F., Berkes C., Williamson P.L.,
 RA Schlegel R.A.;
 RT "Multiple members of a third subfamily of P-type ATPases identified by
 RT genomic sequences and ESTs.";
 RL Genome Res. 8:354-361(1998).
 CC -!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + PHOSPHATE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- TISSUE SPECIFICITY: FOUND IN MOST TISSUES EXCEPT SPLEEN. MOST
 CC ABUNDANT IN BRAIN. ALSO DETECTED IN FETAL TISSUES.
 CC -!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
 CC ATPASES). SUBFAMILY IV.
 CC -----
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 CC -----
 DR EMBL; AF152243; AAF08396.1; -
 DR EMBL; AF011336; AAC05245.1; -
 DR

```
DR MGD; MGI:1330826; Atp9a.
DR InterPro; IPR001757; E1-E2_ATPase.
DR InterPro; IPR001454; Hydrolase.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR001119; CATAPASE.
DR PROSITE; PS00154; ATPASE_E1_E2; 1.
KW Hydrolyase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
KW Multigene family.
FT DOMAIN 1 69 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 70 91 POTENTIAL.
FT DOMAIN 92 96 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 97 119 POTENTIAL.
FT DOMAIN 120 303 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 304 325 POTENTIAL.
FT DOMAIN 326 332 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 333 354 POTENTIAL.
FT DOMAIN 355 841 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 842 862 POTENTIAL.
FT DOMAIN 863 874 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 875 893 POTENTIAL.
FT DOMAIN 894 923 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 924 942 POTENTIAL.
FT DOMAIN 943 949 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 950 972 POTENTIAL.
FT DOMAIN 973 978 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 979 999 POTENTIAL.
FT DOMAIN 1000 1006 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1007 1030 POTENTIAL.
FT MOD_RES 1031 1047 PHOSPHORYLATION (BY SIMILARITY).
FT METAL 785 785 MAGNESIUM (BY SIMILARITY).
FT METAL 789 789 MAGNESIUM (BY SIMILARITY).
FT CONFLICT 29 29 R -> K (IN REF. 2).
FT CONFLICT 129 129 V -> I (IN REF. 2).
FT CONFLICT 138 138 V -> I (IN REF. 2).
FT CONFLICT 278 278 R -> K (IN REF. 2).
FT CONFLICT 432 432 Q -> P (IN REF. 2).
FT CONFLICT 475 475 S -> C (IN REF. 2).
FT CONFLICT 533 533 V -> I (IN REF. 2).
FT CONFLICT 613 613 H -> D (IN REF. 2).
FT CONFLICT 742 742 E -> D (IN REF. 2).
FT CONFLICT 784 784 W -> G (IN REF. 2).
SQ SEQUENCE 1047 AA; 118756 MW; B76AE98C32F6D04 CRC64;

Query Match 3.8%; Score 8; DB 1; Length 1047;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 PELYKDLL 208
DB 907 PELYKDLL 914
|||||||

RESULT 13
ID INFB_HAEIN STANDARD; PRT; 94 AA.
AC P43724;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Integration host factor beta-subunit (IHF-beta).
GN INFB OR HIMD OR H1221.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OC NCB1_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

RA Scott J.D., Shirley R., Liu L.-I., Glodex A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd.";
RL Science 269:496-512(1995).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE TWO SUBUNITS OF INTEGRATION
CC HOST FACTOR, A SPECIFIC DNA-BINDING PROTEIN THAT FUNCTIONS IN
CC GENETIC RECOMBINATION AS WELL AS IN TRANSCRIPTIONAL AND
CC TRANSLATIONAL CONTROL (BY SIMILARITY).
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
CC -----
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CC -----
CC EMBL; U32802; AAC22874.1; -
CC HSSP; P08756; IHF.
DR TIGR; H1221; -.
DR InterPro; IPR000119; Bac_DNA_binding.
DR Pfam; PF00216; Bac_DNA_binding; 1.
DR ProDom; PD000945; Bac_DNA_binding; 1.
DR SMART; SM00411; BHL; 1.
DR PROSITE; PS00045; HISTONE_LIKE; 1.
KW DNA-binding; Transcription regulation; DNA recombination;
KW Translation regulation; Complete proteome.
SQ SEQUENCE 94 AA; 10454 MW; 3EAA97B915B63EAF CRC64;

Query Match 3.3%; Score 7; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 GILEFIS 102
DB 28 GILEFIS 34
|||||||

RESULT 14
ID CEPL_CERFI STANDARD; PRT; 120 AA.
AC P81702;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cerato-platanin.
OS Ceratocystis fimbriata f. sp. platanii.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Microascales; Microasaceae; Ceratocystis.
OX NCB1_TaxID=88771;
RN [1]
RP SEQUENCE, CHARACTERIZATION, AND DISULFIDE BONDS.
RC STRAIN=AF 100;
RX MEDLINE=99386981; PubMed=10455173;
RA Pazzagli L., Cappugi G., Manao G., Camici G., Santini A.,
RA Scala A.;
RT "Purification, characterization, and amino acid sequence of cerato-
RT platanin, a new phytotoxic protein from Ceratocystis fimbriata f.sp.
RT platanii.";
RL J. Biol. Chem. 274:24959-24964(1999).
CC -!- FUNCTION: PHYTOXIN WHICH CAUSES PRODUCTION OF PHYTOALEXIN IN
CC PLATANUS ACERIFOLIA, PLATANUS OCCIDENTALIS AND PLATANUS
CC ORIENTALIS. INDUCES ALSO CELL NECROSIS. BEHAVES AS FUNGAL TOXIN.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=12383.6.; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE CERATO-PLATANIN FAMILY.
```

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KW Toxin.
FT DISULFID 20 57
ET DISULFID 60 115
SQ SEQUENCE 120 AA; 12400 MW; 131E727B02626B48 CRC64;

Query Match 3.3%; Score 7; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 IRGVDSG 116
Db 73 IRGVDSG 79

RESULT 15
GLB1_LUMTE STANDARD; PRT; 142 AA.
AC P08924;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-AUG-1990 (Rel. 15, Last annotation update)
DE Globin I, extracellular (Erythrocyte) (Globin D).
OS Lumbricus terrestris (Common earthworm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Lumbricus.
OX NCBI_TaxID=6398;
RN [1]
RP SEQUENCE.
RX MEDLINE=87137584; PubMed=3546301;
RA Shishikura F., Snow J.W., Gotoh T., Vinogradov S.N., Walz D.A.;
RT "Amino acid sequence of the monomer subunit of the extracellular
hemoglobin of Lumbricus terrestris.";
RL J. Biol. Chem. 262:3123-3131(1987).
CC -!- SUBUNIT: THE EXTRACELLULAR HEMOGLOBIN OF THE EARTHWORM CONSISTS
OF 12 SUBUNITS THAT HAVE A HEXAGONAL BILAYER STRUCTURE WITH A
MOLECULAR WEIGHT NEAR 3.8 MILLION. EACH ONE-TWELFTH SUBUNIT IS
COMPOSED PRIMARILY OF DISULFIDE LINKED TRIMERS (CHAINS A, B,
AND C) AND MONOMERS (CHAIN D).
CC -!- SIMILARITY: TO OTHER WORM GLOBIN SUBUNITS.
DR PIR; A29134; A29134.
DR InterPro; IPR002336; Erythruin.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00611; ERYTHRUORIN.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport.
FT DISULFID 2 131 BY SIMILARITY
SQ SEQUENCE 142 AA; 16129 MW; 87BE8C74D1BBF1BE CRC64;

Query Match 3.3%; Score 7; DB 1; Length 142;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 AAQLAHL 60
Db 84 AAQLAHL 90

Search completed: October 21, 2002, 16:20:14
Job time : 52 secs

```


GenCore version 5.1.1.3

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OM protein - protein search, using sw model

Run on: October 21, 2002, 16:16:01 ; Search time 29 Seconds
(without alignments)
1258.687 Million cell updates/sec

Title: US-09-817-814-2

Perfect score: 211

Sequence: 1 MAPLAEVGGFLGLEGLGQQ.....PRPVDPERVPELYKDLLMYT 211

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

SPREMBL_19.*

1: sp-archaea.*
2: sp-bacteria.*
3: sp-fungi.*
4: sp-human.*
5: sp-invertebrate.*
6: sp-mammal.*
7: sp-mhc.*
8: sp-organelle.*
9: sp-phage.*
10: sp-plant.*
11: sp-rodent.*
12: sp-virus.*
13: sp-vertebrate.*
14: sp-unclassified.*
15: sp-rvirus.*
16: sp-bacteriap.*
17: sp-archaeap.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	40.3	212	11 Q9EST9	Q9est9 rattus norv
2	75	35.5	212	11 Q9ESL9	Q9esl9 mus musculus
3	26	12.3	208	13 Q9PY1	Q9py1 xenopus lae
4	19	9.0	208	6 Q9SL12	Q9sl12 sus scrofa
5	16	7.6	207	11 Q9ESL8	Q9esl8 mus musculus
6	16	7.6	207	11 Q9ERQ5	Q9erq5 mus musculus
7	8	3.8	197	10 Q9SP9	Q9sp9 arabidopsis
8	8	3.8	215	10 Q9M607	Q9m607 vitis ripar
9	8	3.8	226	10 Q64585	Q64585 arabidopsis
10	8	3.8	275	11 Q70128	Q70128 rattus norv
11	8	3.8	545	10 Q9M332	Q9m332 arabidopsis
12	8	3.8	564	2 Q9X2Y5	Q9x2y5 bacillus an
13	8	3.8	964	11 Q922L9	Q922l9 mus musculus
14	7	3.3	70	16 Q9KCM8	Q9kcw8 bacillus ha
15	7	3.3	101	16 Q9PE80	Q9pe80 xylella fas
16	7	3.3	116	2 Q9SLY6	Q9sly6 streptomyce

Q96mi2	homo sapien	17	3.3	128	4	Q96MI2
Q91090	streptomyce	18	3.3	146	2	Q9LO90
Q94k11	streptomyce	19	3.3	148	2	Q9K4K1
Q919r6	pectobacter	20	3.3	149	2	Q9L9R6
Q9nv89	homo sapien	21	3.3	158	4	Q9NV89
Q61233	lumbricus t	22	3.3	158	5	Q61233
Q61234	lumbricus t	23	3.3	158	5	Q61234
Q99yl7	streptococc	24	3.3	160	16	Q99YL7
Q97nu6	streptococc	25	3.3	167	16	Q97NU6
Q97614	sulfolobus	26	3.3	168	17	Q97614
Q9evb4	streptococc	27	3.3	170	2	Q9EVB4
Q9kut4	vibrio chol	28	3.3	177	16	Q9KUT4
Q9fpp1	amphidinium	29	3.3	188	10	Q9FPP1
Q9axm8	amphidinium	30	3.3	188	10	Q9AXM8
Q9dqp9	human immun	31	3.3	206	15	Q9DQP9
Q97962	human immun	32	3.3	209	15	Q97962
O84742	chlamydia t	33	3.3	219	16	O84742
Q9pli9	chlamydia m	34	3.3	219	16	Q9PLI9
Q9ji98	mus musculus	35	3.3	232	11	Q9Ji98
O19985	arabidopsis	36	3.3	236	8	O19985
O81717	arabidopsis	37	3.3	236	10	O81717
O49915	oryza sativ	38	3.3	238	10	O49915
Q9ft78	arabidopsis	39	3.3	241	10	Q9FT78
Q9c239	neutrospora	40	3.3	246	3	Q9C239
Q96983	human herpe	41	3.3	250	12	Q69083
Q9zbe6	mycobacteri	42	3.3	251	16	Q9ZBE6
Q53033	rhodospirill	43	3.3	255	2	Q53033
O81288	arabidopsis	44	3.3	262	10	O81288
Q9ycr5	aeropyrum p	45	3.3	267	17	Q9YCR5
Q33182	mycobacteri	46	3.3	274	16	Q33182
O91105	pseudomonas	47	3.3	278	16	O91105
Q986u9	rhizobium l	48	3.3	298	16	Q986U9
Q9ae56	rhodococcus	49	3.3	304	2	Q9AE56
Q91183	streptomyce	50	3.3	312	2	Q9L183
Q93qz0	clostridium	51	3.3	312	2	Q93QZ0
P74157	synecocyst	52	3.3	314	16	P74157
Q9nt28	homo sapien	53	3.3	316	4	Q9NT28
O17822	caenorhabdl	54	3.3	316	5	O17822
Q9ha72	homo sapien	55	3.3	323	4	Q9HA72
Q9if38	neisseria m	56	3.3	329	2	Q9IF38
O69662	mycobacteri	57	3.3	330	16	O69662
Q9sp45	jonopsidium	58	3.3	381	10	Q9SP45
Q9sp44	jonopsidium	59	3.3	387	10	Q9SP44
Q9k7z6	bacillus ha	60	3.3	388	16	Q9K7Z6
Q83618	mumps virus	61	3.3	391	12	Q83618
Q9dqa3	mumps virus	62	3.3	391	12	Q9DQA3
Q94416	mumps virus	63	3.3	391	12	Q9J4L6
Q910s3	mumps virus	64	3.3	391	12	Q910S3
O67276	aquifex aeo	65	3.3	392	16	O67276
Q60198	escherichia	66	3.3	400	2	Q60198
Q9uhr0	homo sapien	67	3.3	414	4	Q9UHR0
Q9hbh8	homo sapien	68	3.3	414	4	Q9HBH8
O41607	human immun	69	3.3	418	15	O41607
O41608	human immun	70	3.3	418	15	O41608
Q9x6el	photobacter	71	3.3	420	2	Q9X6E1
O76831	caenorhabdl	72	3.3	425	5	O76831
Q991i3	mus musculus	73	3.3	427	11	Q99LI3
Q9klq8	vibrio chol	74	3.3	436	16	Q9KLQ8
Q9ycw5	aeropyrum p	75	3.3	439	17	Q9YCW5
P94647	chlorobium	76	3.3	474	2	P94647
Q53032	rhodospirill	77	3.3	480	2	Q53032
Q9a595	caulobacter	78	3.3	486	16	Q9A595
Q99988	herpes simp	79	3.3	486	12	Q99988
Q97kc0	clostridium	80	3.3	496	16	Q97KC0
Q9j0x9	human herpe	81	3.3	512	12	Q9J0X9
Q92pp7	rhizobium m	82	3.3	549	16	Q92PP7
O64069	bacterioph	83	3.3	589	16	O64069
O31952	bacillus su	84	3.3	589	16	O31952
Q9fbis	streptomyce	85	3.3	593	2	Q9FBIS
Q92lu9	mus musculus	86	3.3	626	11	Q92LU9
Q9w556	drosophila	87	3.3	631	5	Q9W556
Q9bh9	homo sapien	88	3.3	637	4	Q9BH9
Q93gz5	streptomyce	89	3.3	641	2	Q93GZ5

90	7	3.3	657	10	023427	023427 arabidopsis	163	6	2.8	82	12	09YJ13	09YJ13 encephalomy
91	7	3.3	676	13	09DGC7	Q9dgc7 brachydanio	164	6	2.8	82	12	09WK34	Q9wk34 encephalomy
92	7	3.3	678	5	Q9V3Q6	Q9v3q6 drosophila	165	6	2.8	82	12	09WK33	Q9wk33 encephalomy
93	7	3.3	703	2	09L3P4	Q9l3p4 uncultured	166	6	2.8	82	12	09YPK8	Q9ypk8 encephalomy
94	7	3.3	711	4	09H123	Q9h123 homo sapien	167	6	2.8	82	12	09YPK7	Q9ypk7 encephalomy
95	7	3.3	711	4	Q96K25	Q96k25 homo sapien	168	6	2.8	82	12	09YPK5	Q9ypk5 encephalomy
96	7	3.3	711	4	Q96K24	Q96k24 homo sapien	169	6	2.8	84	12	Q91EQ2	Q91eq2 dengue viru
97	7	3.3	738	10	Q9M0Z0	Q9m0z0 arabidopsis	170	6	2.8	86	16	Q97LR6	Q97lk6 clostridium
98	7	3.3	743	10	Q93V99	Q93v99 arabidopsis	171	6	2.8	88	2	Q9S590	Q9s590 nitrosomona
99	7	3.3	757	4	Q9UFA2	Q9ufa2 homo sapien	172	6	2.8	88	15	Q9WCP3	Q9wcp3 human immun
100	7	3.3	757	5	Q960E5	Q960e5 drosophila	173	6	2.8	89	4	Q16343	Q16343 homo sapien
101	7	3.3	772	10	Q9ZPH7	Q9zph7 arabidopsis	174	6	2.8	90	10	Q9ZVC5	Q9zvc5 arabidopsis
102	7	3.3	782	5	Q9NIS1	Q9nisl drosophila	175	6	2.8	90	17	Q97CT1	Q97ct1 thermoplasm
103	7	3.3	783	5	Q9VF04	Q9vft4 drosophila	176	6	2.8	90	17	Q97I24	Q97i24 sulfolobus
104	7	3.3	812	2	Q9FBT4	Q9fbt4 streptomyce	177	6	2.8	91	5	Q9NBJ9	Q9nbj9 caenorhabdi
105	7	3.3	815	2	030740	Q30740 rhodobacter	178	6	2.8	91	17	Q9UY47	Q9uy47 pyrococcus
106	7	3.3	829	16	Q9KLR4	Q9klr4 vibrio chol	179	6	2.8	93	12	Q98335	Q98335 macroptiliu
107	7	3.3	829	16	Q9KLR4	Q9klr4 vibrio chol	180	6	2.8	93	12	Q98335	Q98335 macroptiliu
108	7	3.3	831	2	Q9H143	Q9h143 pseudomonas	181	6	2.8	95	12	Q98443	Q98443 paramecium
109	7	3.3	834	2	Q9Z3W4	Q9z3w4 pseudomonas	182	6	2.8	95	15	Q99DE3	Q99de3 human immun
110	7	3.3	834	16	Q9Z236	Q9z236 rhizobium m	183	6	2.8	96	10	Q41900	Q41900 arabidopsis
111	7	3.3	853	2	Q9RC05	Q9rc05 pseudomonas	184	6	2.8	96	15	Q9DHC0	Q9dhc0 human immun
112	7	3.3	875	16	Q9ZPM5	Q9zpm5 rhizobium m	185	6	2.8	96	15	Q9DHC0	Q9dhc0 human immun
113	7	3.3	917	4	Q9H698	Q9h698 homo sapien	186	6	2.8	96	15	Q9DHC0	Q9dhc0 human immun
114	7	3.3	917	4	Q9H698	Q9h698 homo sapien	187	6	2.8	96	15	Q9DHC0	Q9dhc0 human immun
115	7	3.3	955	4	Q96DN2	Q96dn2 homo sapien	188	6	2.8	97	2	Q930U5	Q930u5 agrobacteri
116	7	3.3	1012	5	Q76903	Q76903 drosophila	189	6	2.8	97	15	Q99DD3	Q99dd3 human immun
117	7	3.3	1025	2	Q54507	Q54507 streptococc	190	6	2.8	98	2	Q9XDH1	Q9xdh1 streptomyce
118	7	3.3	1025	2	P72532	P72532 streptococc	191	6	2.8	98	4	Q9BZH7	Q9bzh7 homo sapien
119	7	3.3	1058	5	Q9VK04	Q9vk04 drosophila	192	6	2.8	98	10	Q9XFT7	Q9xft7 chlamydomon
120	7	3.3	1058	16	Q930F6	Q930f6 rhizobium m	193	6	2.8	99	3	Q9C225	Q9c225 neurospora
121	7	3.3	1120	5	Q9VUK6	Q9vuk6 drosophila	194	6	2.8	99	10	Q9ZVC4	Q9zvc4 arabidopsis
122	7	3.3	1152	3	Q9UUY1	Q9uuy1 neurospora	195	6	2.8	100	16	Q9MFD1	Q9mfd1 beta vulgar
123	7	3.3	1267	13	Q98945	Q98945 gallus gall	196	6	2.8	100	16	Q9MDK6	Q9mdk6 rhizobium l
124	7	3.3	1326	2	Q9L2C3	Q9l2c3 streptomyce	197	6	2.8	100	17	Q9YD29	Q9yvd29 aeropyrum p
125	7	3.3	1331	3	Q9HED0	Q9hed0 neurospora	198	6	2.8	101	2	Q9R413	Q9r413 ureaplasma
126	7	3.3	1339	4	Q75276	Q75276 homo sapien	199	6	2.8	101	2	Q9R7K9	Q9r7k9 ureaplasma
127	7	3.3	1418	16	Q9RRW1	Q9rrw1 deinococcus	200	6	2.8	101	2	Q9R7K8	Q9r7k8 ureaplasma
128	7	3.3	1530	5	Q9NH11	Q9nh11 drosophila	201	6	2.8	101	2	Q9R7K7	Q9r7k7 ureaplasma
129	7	3.3	1536	3	Q06625	Q06625 saccharomyc	202	6	2.8	101	2	Q9R7K6	Q9r7k6 ureaplasma
130	7	3.3	1536	3	Q93808	Q93808 saccharomyc	203	6	2.8	101	2	Q9R7K5	Q9r7k5 ureaplasma
131	7	3.3	1579	5	Q9VSE6	Q9vse6 drosophila	204	6	2.8	101	2	Q9R7K4	Q9r7k4 ureaplasma
132	7	3.3	1581	4	Q94911	Q94911 homo sapien	205	6	2.8	101	2	Q9R7K3	Q9r7k3 ureaplasma
133	7	3.3	1607	5	Q94599	Q94599 leishmania	206	6	2.8	101	2	Q9R7K2	Q9r7k2 ureaplasma
134	7	3.3	1778	5	Q9NE65	Q9ne65 leishmania	207	6	2.8	101	2	Q9RFB0	Q9rfb0 streptomyce
135	7	3.3	2163	5	Q01912	Q01912 caenorhabdi	208	6	2.8	101	2	Q03336	Q03336 alcaligenes
136	7	3.3	3390	12	Q99D35	Q99d35 dengue viru	209	6	2.8	101	2	Q93T82	Q93t82 bruceella ab
137	7	3.3	3638	4	Q15142	Q15142 homo sapien	210	6	2.8	101	8	Q9BAC0	Q9bac0 euglena ste
138	7	3.3	4292	4	Q15141	Q15141 homo sapien	211	6	2.8	101	10	Q94LA6	Q94la6 arabidopsis
139	7	3.3	4302	4	Q15140	Q15140 homo sapien	212	6	2.8	101	17	Q97ZL0	Q97z10 sulfolobus
140	7	3.3	13055	5	Q9165	Q9165 caenorhabdi	213	6	2.8	103	2	Q9Z376	Q9z376 actinomycetes
141	6	2.8	22	2	Q9R5C0	Q9r5c0 nitrosomona	214	6	2.8	103	10	Q9SYR2	Q9syrr2 artica diol
142	6	2.8	27	10	Q9S8M4	Q9s8m4 avena sativ	215	6	2.8	105	2	Q9RZW7	Q9rzw7 borrelia bu
143	6	2.8	49	12	Q91FK3	Q91fk3 chilo iride	216	6	2.8	106	2	Q87401	Q87401 synchococc
144	6	2.8	51	4	Q9UJ11	Q9uj11 homo sapien	217	6	2.8	106	4	Q9UN93	Q9un93 homo sapien
145	6	2.8	61	16	Q92WL2	Q92wl2 rhizobium m	218	6	2.8	106	16	Q92H48	Q92h48 rickettsia
146	6	2.8	64	10	Q42983	Q42983 oryza sativ	219	6	2.8	106	16	Q64841	Q64841 arabidopsis
147	6	2.8	64	16	Q9PD64	Q9pd64 xyella fas	220	6	2.8	108	11	Q9D2X4	Q9d2x4 mus musculu
148	6	2.8	65	2	Q47784	Q47784 enterococcu	221	6	2.8	108	15	Q9QN68	Q9qn68 human immun
149	6	2.8	65	2	Q91658	Q91658 enterococcu	222	6	2.8	108	15	Q10826	Q10826 human immun
150	6	2.8	66	11	Q9Z5P4	Q9z5p4 mus musculu	223	6	2.8	111	2	Q9FBX9	Q9fbx9 streptomyce
151	6	2.8	67	2	Q54576	Q54576 streptococc	224	6	2.8	111	2	Q9ACQ0	Q9acq0 streptomyce
152	6	2.8	68	2	Q83015	Q83015 streptomyce	225	6	2.8	111	12	Q85304	Q85304 orf viru
153	6	2.8	70	7	Q95194	Q95194 stizostedio	226	6	2.8	112	2	Q9R1W3	Q9r1w3 streptomyce
154	6	2.8	70	7	Q95192	Q95192 stizostedio	227	6	2.8	112	10	Q9S7W3	Q9s7w3 artica diol
155	6	2.8	70	7	Q95191	Q95191 stizostedio	228	6	2.8	112	10	Q9S7K1	Q9s7k1 artica diol
156	6	2.8	70	7	Q95188	Q95188 stizostedio	229	6	2.8	112	10	Q9S7B3	Q9s7b3 artica diol
157	6	2.8	70	7	Q95183	Q95183 stizostedio	230	6	2.8	112	10	Q9S705	Q9s705 artica diol
158	6	2.8	73	10	Q9M5K8	Q9m5k8 zea mays (m	231	6	2.8	112	10	Q9ZP51	Q9zps1 artica diol
159	6	2.8	78	9	Q94MY7	Q94my7 haemophilus	232	6	2.8	112	10	Q9SYR5	Q9syrs5 artica diol
160	6	2.8	82	12	Q9YJ99	Q9yj99 encephalomy	233	6	2.8	112	15	Q75730	Q75730 human immun
161	6	2.8	82	12	Q9YJ06	Q9yj06 encephalomy	234	6	2.8	112	15	Q75731	Q75731 human immun
162	6	2.8	82	12	Q9YJMI	Q9yjmi encephalomy	235	6	2.8	112	17	Q972S1	Q972s1 sulfolobus

236	6	2.8	113	10	Q9S7C2	Q9S7C2 urtica dioi	309	6	2.8	146	16	Q92X66	Q92X66 rhizobium m
237	6	2.8	114	10	Q9AST5	Q9ast5 arabidopsis	310	6	2.8	148	12	Q9YLA6	Q9yla6 macrophilia
238	6	2.8	115	2	Q00605	Q00605 streptococc	311	6	2.8	148	17	Q9V252	Q9v252 pyrococcus
239	6	2.8	116	15	Q97005	Q97005 human immun	312	6	2.8	149	2	Q9L9T5	Q9l9t5 brenneria r
240	6	2.8	117	11	Q9D3K8	Q9d3k8 mus musculu	313	6	2.8	149	2	Q9L9T3	Q9l9t3 brenneria r
241	6	2.8	118	15	Q70199	Q70199 human immun	314	6	2.8	149	2	Q9L9T2	Q9l9t2 brenneria r
242	6	2.8	116	15	O40241	O40241 human immun	315	6	2.8	149	2	Q9RI11	Q9ri11 yersinia pe
243	6	2.8	116	15	O40242	O40242 human immun	316	6	2.8	149	5	Q25383	Q25383 loligo peal
244	6	2.8	116	15	Q97007	Q97007 human immun	317	6	2.8	149	12	P88975	P88975 macrophilia
245	6	2.8	117	2	Q9F8Z8	Q9f8z8 streptococc	318	6	2.8	151	12	P88893	P88893 jamaican to
246	6	2.8	117	16	Q99T85	Q99t85 staphylococ	319	6	2.8	152	8	O48119	O48119 ungaliophis
247	6	2.8	118	8	Q35595	Q35595 physarum po	320	6	2.8	152	15	Q9DRS6	Q9drs6 human immun
248	6	2.8	118	15	O41584	O41584 human immun	321	6	2.8	152	16	Q9A2T9	Q9a2t9 caulobacter
249	6	2.8	120	15	O41592	O41592 human immun	322	6	2.8	153	2	Q9EWY1	Q9ewy1 streptomyc
250	6	2.8	121	11	Q99LY5	Q99ly5 mus musculu	323	6	2.8	153	10	Q9LW8	Q9lw8 oryza sativ
251	6	2.8	121	15	Q76348	Q76348 human immun	324	6	2.8	153	12	O41475	O41475 weissadula g
252	6	2.8	121	15	Q97986	Q97986 human immun	325	6	2.8	153	15	Q74916	Q74916 human immun
253	6	2.8	121	17	Q9YAA1	Q9yaal aeropyrum p	326	6	2.8	153	16	Q982G4	Q982g4 rhizobium l
254	6	2.8	122	4	Q9UFS1	Q9ufsl homo sapien	327	6	2.8	154	11	Q63847	Q63847 mus musculu
255	6	2.8	122	5	Q9TYV6	Q9tyv6 caenorhabdi	328	6	2.8	154	15	P88419	P88419 human immun
256	6	2.8	122	6	Q95KC2	Q95kc2 macaca fasc	329	6	2.8	155	2	O85238	O85238 yersinia en
257	6	2.8	123	2	Q50766	Q50766 mycobacteri	330	6	2.8	155	15	P88431	P88431 human immun
258	6	2.8	123	15	Q9QM82	Q9qm82 human immun	331	6	2.8	155	15	Q9Q5H0	Q9q5h0 human immun
259	6	2.8	123	15	Q85587	Q85587 aids-associ	332	6	2.8	157	15	Q9Q5G9	Q9q5g9 human immun
260	6	2.8	124	11	Q9D179	Q9d179 mus musculu	333	6	2.8	157	15	Q9Q5G9	Q9q5g9 human immun
261	6	2.8	124	13	Q90XQ5	Q90xq5 ambystoma m	334	6	2.8	159	5	Q9BHK1	Q9bhl1 sabella spa
262	6	2.8	124	16	Q9KG60	Q9kg60 bacillus ha	335	6	2.8	159	8	Q9MG06	Q9mg06 haemoproteu
263	6	2.8	125	6	Q9SK85	Q9sk85 macaca fasc	336	6	2.8	159	8	Q9MG05	Q9mg05 haemoproteu
264	6	2.8	129	4	O43180	O43180 homo sapien	337	6	2.8	159	8	Q9MG04	Q9mg04 haemoproteu
265	6	2.8	129	4	Q96MT5	Q96mt5 homo sapien	338	6	2.8	159	8	Q9MG03	Q9mg03 haemoproteu
266	6	2.8	129	11	Q9CVD0	Q9cvd0 mus musculu	339	6	2.8	159	8	Q9MG02	Q9mg02 haemoproteu
267	6	2.8	129	15	Q9QRB0	Q9qrb0 human immun	340	6	2.8	159	8	Q9MG01	Q9mg01 haemoproteu
268	6	2.8	130	2	Q50753	Q50753 mycobacteri	341	6	2.8	159	8	Q9MG00	Q9mg00 haemoproteu
269	6	2.8	131	2	Q9AIK9	Q9aik9 pseudomonas	342	6	2.8	159	8	Q9MEF7	Q9mfz7 haemoproteu
270	6	2.8	131	5	Q9V5V5	Q9v5v5 pseudophila	343	6	2.8	159	8	Q9MEF24	Q9mfz4 haemoproteu
271	6	2.8	131	17	Q9YBW3	Q9ybw3 aeropyrum p	344	6	2.8	159	10	Q9FGZ2	Q9fgz2 arabidopsis
272	6	2.8	132	10	Q9FWG9	Q9fwg9 oryza sativ	345	6	2.8	160	16	Q97SJ9	Q97sj9 streptococ
273	6	2.8	132	10	Q9FU43	Q9fu43 oryza sativ	346	6	2.8	161	2	Q9RMA8	Q9rma8 bacillus ci
274	6	2.8	132	12	Q91E07	Q91eq7 dengue viru	347	6	2.8	162	12	O09723	O09723 bean golden
275	6	2.8	132	12	Q91E06	Q91eq6 dengue viru	348	6	2.8	162	15	Q9WIR1	Q9wir1 human immun
276	6	2.8	132	12	Q91EQ5	Q91eq5 dengue viru	349	6	2.8	162	15	Q9WIR3	Q9wir3 human immun
277	6	2.8	132	12	Q91EQ4	Q91eq4 dengue viru	350	6	2.8	163	17	Q9VLI9	Q9vli9 pyrococcus
278	6	2.8	132	12	Q91EQ3	Q91eq3 dengue viru	351	6	2.8	164	4	Q9NSJ2	Q9nsj2 homo sapien
279	6	2.8	133	8	Q36308	Q36308 adalia bipu	352	6	2.8	164	16	Q9AB51	Q9ab51 caulobacter
280	6	2.8	133	16	O07760	O07760 mycobacteri	353	6	2.8	165	2	Q9K3X8	Q9k3x8 streptomyc
281	6	2.8	134	2	Q9XB26	Q9xb26 klebsiella	354	6	2.8	165	5	Q966T8	Q966t8 bombyx mori
282	6	2.8	134	12	Q9QD36	Q9qdj6 tomato yell	355	6	2.8	165	17	Q9XE68	Q9xe68 aeropyrum p
283	6	2.8	135	15	Q9PWX9	Q9pwx9 human immun	356	6	2.8	166	10	Q9AK31	Q9ak31 arabidopsis
284	6	2.8	135	15	Q9QMF6	Q9qmf6 human immun	357	6	2.8	166	16	Q9JXX9	Q9jxx9 neisseria m
285	6	2.8	136	4	Q9UGZ2	Q9ugz2 homo sapien	358	6	2.8	166	16	Q9JVZ1	Q9jvz1 neisseria m
286	6	2.8	136	16	Q99RY3	Q99ry3 staphylococ	359	6	2.8	167	15	Q9YKS7	Q9yks7 human immun
287	6	2.8	137	15	Q94AU5	Q94au5 arabidopsis	360	6	2.8	168	16	Q92Y45	Q92y45 rhizobium m
288	6	2.8	137	15	Q9DRS8	Q9drs8 human immun	361	6	2.8	169	2	Q9X778	Q9x778 mycobacteri
289	6	2.8	138	1	Q9HH46	Q9hh46 methanobact	362	6	2.8	169	12	Q917Q8	Q917q8 hepatitis c
290	6	2.8	138	2	Q9X3A6	Q9x3a6 unidentifie	363	6	2.8	170	12	Q65868	Q65868 barley yell
291	6	2.8	139	10	Q9XFE8	Q9xfe8 oryza sativ	364	6	2.8	170	17	Q980V4	Q980v4 sulfolobus
292	6	2.8	139	15	Q9DRR3	Q9drr3 human immun	365	6	2.8	171	5	Q9USB3	Q9usb3 caenorhabdi
293	6	2.8	139	15	Q79687	Q79687 human immun	366	6	2.8	171	16	Q916L4	Q916l4 pseudomonas
294	6	2.8	140	11	Q62990	Q62990 rattus norv	367	6	2.8	172	2	Q9RGM9	Q9rgm9 neisseria g
295	6	2.8	140	15	Q9DHB8	Q9dhb8 human immun	368	6	2.8	172	11	Q9D7B4	Q9d7b4 mus musculu
296	6	2.8	140	15	Q9Q5D4	Q9q5d4 human immun	369	6	2.8	173	5	Q93209	Q93209 caenorhabdi
297	6	2.8	140	15	Q9DRR5	Q9drr5 human immun	370	6	2.8	174	2	Q9AD00	Q9ad00 streptomyc
298	6	2.8	140	15	Q9DRR4	Q9drr4 human immun	371	6	2.8	175	2	O50239	O50239 zymomonas m
299	6	2.8	140	15	Q9WIN0	Q9win0 human immun	372	6	2.8	175	4	Q9NKS5	Q9nks5 homo sapien
300	6	2.8	140	15	O10839	O10839 human immun	373	6	2.8	176	2	Q93IK6	Q93ik6 vibrio sp.
301	6	2.8	142	2	Q9ZGX5	Q9zgx5 yersinia pe	374	6	2.8	176	15	Q74918	Q74918 human immun
302	6	2.8	142	12	Q66762	Q66762 encephalomy	375	6	2.8	177	2	Q9RJI1	Q9rjl1 streptomyc
303	6	2.8	143	2	Q93OE1	Q93qe1 streptococc	376	6	2.8	177	2	Q9EXJ7	Q9exj7 escherichia
304	6	2.8	143	10	Q9FRF4	Q9frf4 oryza sativ	377	6	2.8	179	10	Q94J05	Q94ju5 arabidopsis
305	6	2.8	143	16	Q9ZN07	Q9zn07 helicobacte	378	6	2.8	179	11	Q9CYC1	Q9cyc1 mus musculu
306	6	2.8	144	16	O25745	O25745 helicobacte	379	6	2.8	180	2	Q9RJM3	Q9rjm3 streptomyc
307	6	2.8	144	16	Q9ZK93	Q9zk93 helicobacte	380	6	2.8	180	16	Q91766	Q91766 pseudomonas
308	6	2.8	146	12	Q9Q2O6	Q9q2q6 human papil	381	6	2.8	181	2	Q92MY1	Q92my1 rhizobium m
												Q9XBW7	Q9xbw7 rhodobacter

382	6	2.8	181	10	Q9XGT3	Q9xgt3 vitis vinif	455	6	2.8	200	15	Q79789	Q79789 human immun
383	6	2.8	181	15	Q9DRP1	Q9drp1 human immun	456	6	2.8	200	15	Q74842	Q74842 human immun
384	6	2.8	182	5	Q9W1r7	Q9w1r7 drosophila	457	6	2.8	200	15	Q75147	Q75147 human immun
385	6	2.8	182	15	Q80820	Q80820 human t-cel	458	6	2.8	201	15	Q9YYU8	Q9yyu8 human immun
386	6	2.8	182	15	Q85574	Q85574 aids-associ	459	6	2.8	201	15	Q9QRL7	Q9qrl7 human immun
387	6	2.8	182	16	Q98M88	Q98m88 rhizobium l	460	6	2.8	201	15	Q9QRL6	Q9qrl6 human immun
388	6	2.8	183	4	Q9NUS6	Q9nus6 homo sapien	461	6	2.8	201	15	Q9QRL5	Q9qrl5 human immun
389	6	2.8	183	15	Q9DRU1	Q9drul human immun	462	6	2.8	201	15	Q9QRL4	Q9qrl4 human immun
390	6	2.8	183	15	Q9KSC5	Q9ksc5 vibrio chol	463	6	2.8	201	15	Q9QRL3	Q9qrl3 human immun
391	6	2.8	184	15	Q9DRS7	Q9drs7 human immun	464	6	2.8	201	15	Q9QRL2	Q9qrl2 human immun
392	6	2.8	184	16	Q9RSY8	Q9rsy8 delinococcus	465	6	2.8	202	12	Q9Z097	Q9z097 tobacco lea
393	6	2.8	184	16	Q9RIIS6	Q9riis6 pseudomonas	466	6	2.8	202	15	Q72622	Q72622 human immun
394	6	2.8	185	2	Q9R8R4	Q9r8r4 helicobacte	467	6	2.8	202	15	Q9QPN3	Q9qpn3 human immun
395	6	2.8	185	2	Q9R8R2	Q9r8r2 helicobacte	468	6	2.8	202	15	Q91022	Q91022 human immun
396	6	2.8	185	2	Q9S229	Q9s229 streptomyce	469	6	2.8	202	15	Q75748	Q75748 human immun
397	6	2.8	185	4	Q9BX24	Q9bx24 homo sapien	470	6	2.8	202	15	P90279	P90279 human immun
398	6	2.8	185	5	Q45206	Q45206 schistosoma	471	6	2.8	202	15	P88435	P88435 human immun
399	6	2.8	185	12	Q98693	Q98693 sida golden	472	6	2.8	203	15	Q9FX46	Q9fx46 human immun
400	6	2.8	187	2	Q4805	Q4805 streptococc	473	6	2.8	203	15	Q9FX37	Q9fx37 human immun
401	6	2.8	188	2	Q9L031	Q9l031 streptomyce	474	6	2.8	203	15	Q9PFW2	Q9pww2 human immun
402	6	2.8	188	12	Q9IMV3	Q9imv3 beet wester	475	6	2.8	203	15	Q9QND7	Q9qnd7 human immun
403	6	2.8	188	15	Q9WM27	Q9wm27 human immun	476	6	2.8	203	15	Q9QND6	Q9qnd6 human immun
404	6	2.8	189	16	Q34643	Q34643 bacillus su	477	6	2.8	203	15	Q9QND5	Q9qnd5 human immun
405	6	2.8	190	12	Q9W827	Q9w827 tobacco lea	478	6	2.8	203	15	Q9QND4	Q9qnd4 human immun
406	6	2.8	190	12	Q9Z0A7	Q9z0a7 tobacco lea	479	6	2.8	203	15	Q9QND3	Q9qnd3 human immun
407	6	2.8	190	12	Q9Z095	Q9z095 tobacco lea	480	6	2.8	203	15	Q9QND2	Q9qnd2 human immun
408	6	2.8	190	12	Q9Z089	Q9z089 tobacco lea	481	6	2.8	203	15	Q9QND1	Q9qnd1 human immun
409	6	2.8	190	12	Q9Z086	Q9z086 tobacco lea	482	6	2.8	203	15	Q9QNC8	Q9qnc8 human immun
410	6	2.8	190	12	Q9Z084	Q9z084 tobacco lea	483	6	2.8	203	15	Q9QNC6	Q9qnc6 human immun
411	6	2.8	190	12	Q9Z081	Q9z081 tobacco lea	484	6	2.8	203	15	Q9QNC6	Q9qnc6 human immun
412	6	2.8	191	4	Q9HAF1	Q9haf1 homo sapien	485	6	2.8	203	15	Q9QNC5	Q9qnc5 human immun
413	6	2.8	191	10	Q94LF2	Q94lf2 oryza sativ	486	6	2.8	203	15	Q9QNC4	Q9qnc4 human immun
414	6	2.8	191	13	Q9DFC9	Q9dfc9 brachydanio	487	6	2.8	203	15	Q9QNC3	Q9qnc3 human immun
415	6	2.8	191	17	Q9HQH3	Q9hgh3 halobacteri	488	6	2.8	203	15	Q9QNC2	Q9qnc2 human immun
416	6	2.8	192	11	Q9D7J5	Q9d7j5 mus musculu	489	6	2.8	203	15	Q9QNC1	Q9qnc1 human immun
417	6	2.8	192	15	Q9WIR2	Q9wir2 human immun	490	6	2.8	203	15	Q9QNC0	Q9qnc0 human immun
418	6	2.8	192	15	Q9WIR4	Q9wir4 human immun	491	6	2.8	203	15	Q9QNC5	Q9qnc5 human immun
419	6	2.8	192	15	Q9YNB9	Q9ynb9 human immun	492	6	2.8	203	15	Q9QNC7	Q9qnc7 human immun
420	6	2.8	192	15	Q9YNB8	Q9ynb8 human immun	493	6	2.8	203	15	Q9QNC5	Q9qnc5 human immun
421	6	2.8	192	15	Q9YNE7	Q9yne7 human immun	494	6	2.8	203	15	Q9IQX7	Q9iqx7 human immun
422	6	2.8	193	10	Q9ASF1	Q9asf1 oryza sativ	495	6	2.8	203	15	Q9IQX6	Q9iqx6 human immun
423	6	2.8	193	11	Q9ES34	Q9es34 mus musculu	496	6	2.8	203	15	Q9IQX5	Q9iqx5 human immun
424	6	2.8	194	2	Q9S406	Q9s406 proteus mir	497	6	2.8	203	15	Q9IQX4	Q9iqx4 human immun
425	6	2.8	194	15	Q9WPY0	Q9wpy0 human immun	498	6	2.8	203	15	Q9QMF5	Q9qmf5 human immun
426	6	2.8	195	4	Q9H7R4	Q9h7r4 homo sapien	499	6	2.8	203	15	Q9QMF4	Q9qmf4 human immun
427	6	2.8	196	11	Q9JK08	Q9jkc8 mus musculu	500	6	2.8	203	15	Q90523	Q90523 human immun
428	6	2.8	196	13	Q9YH31	Q9yh31 notophthalm	501	6	2.8	203	15	Q9QRH3	Q9qrh3 human immun
429	6	2.8	197	12	Q65880	Q65880 barley yell	502	6	2.8	203	15	Q9WPS5	Q9wps5 human immun
430	6	2.8	197	15	Q10816	Q10816 human immun	503	6	2.8	203	15	Q9JAC0	Q9jac0 human immun
431	6	2.8	197	15	Q10817	Q10817 human immun	504	6	2.8	203	15	Q9DRX1	Q9drx1 human immun
432	6	2.8	197	15	Q10818	Q10818 human immun	505	6	2.8	203	15	Q9DRX0	Q9drx0 human immun
433	6	2.8	197	15	Q10820	Q10820 human immun	506	6	2.8	203	15	Q9DRW9	Q9drw9 human immun
434	6	2.8	197	15	Q10822	Q10822 human immun	507	6	2.8	203	15	Q9DRW8	Q9drw8 human immun
435	6	2.8	197	15	Q10824	Q10824 human immun	508	6	2.8	203	15	Q9DRW7	Q9drw7 human immun
436	6	2.8	197	15	Q10827	Q10827 human immun	509	6	2.8	203	15	Q72471	Q72471 human immun
437	6	2.8	197	15	Q10828	Q10828 human immun	510	6	2.8	203	15	Q74926	Q74926 human immun
438	6	2.8	197	15	Q10829	Q10829 human immun	511	6	2.8	203	15	Q75724	Q75724 human immun
439	6	2.8	197	15	Q10829	Q10829 human immun	512	6	2.8	203	15	Q75725	Q75725 human immun
440	6	2.8	197	15	Q04021	Q04021 human immun	513	6	2.8	203	15	Q902Q5	Q902q5 human immun
441	6	2.8	198	2	Q50927	Q50927 nitrosomona	514	6	2.8	203	15	Q902I3	Q902i3 human immun
442	6	2.8	198	15	Q9DRV2	Q9drv2 human immun	515	6	2.8	203	15	Q901T9	Q901t9 human immun
443	6	2.8	198	15	Q9DRU9	Q9dru9 human immun	516	6	2.8	204	12	Q9Z091	Q9z091 tobacco lea
444	6	2.8	198	15	Q9DRU8	Q9dru8 human immun	517	6	2.8	204	15	Q89665	Q89665 human immun
445	6	2.8	198	15	Q9DRU7	Q9dru7 human immun	518	6	2.8	204	15	Q9PXA5	Q9pxa5 human immun
446	6	2.8	198	15	Q9DRG2	Q9drg2 human immun	519	6	2.8	204	15	Q9PXA5	Q9pxa5 human immun
447	6	2.8	198	15	Q74906	Q74906 human immun	520	6	2.8	204	15	Q9PX78	Q9px78 human immun
448	6	2.8	198	15	Q74907	Q74907 human immun	521	6	2.8	204	15	Q9PX09	Q9px09 human immun
449	6	2.8	198	15	Q74908	Q74908 human immun	522	6	2.8	204	15	Q91CH2	Q91ch2 human immun
450	6	2.8	199	8	Q94R62	Q94r62 vipera beru	523	6	2.8	204	15	Q9D6X7	Q9d6x7 human immun
451	6	2.8	199	15	Q9DRV1	Q9drv1 human immun	524	6	2.8	204	15	Q73570	Q73570 human immun
452	6	2.8	199	15	Q76351	Q76351 human immun	525	6	2.8	204	15	Q91R12	Q91r12 human immun
453	6	2.8	200	2	Q9AD73	Q9ad73 streptomyce	526	6	2.8	204	15	Q91R11	Q91r11 human immun
454	6	2.8	200	2	Q93F35	Q93f35 shigella fl	527	6	2.8	204	15	Q91R10	Q91r10 human immun
						Q90071 human immun						Q92803	Q92803 human immun

528	6	2.8	204	15	071125	071125 human immun	601	6	2.8	205	15	09WPV6	09WPV6 human immun
529	6	2.8	204	15	071127	071127 human immun	602	6	2.8	205	15	09WPV2	09WPV2 human immun
530	6	2.8	204	15	Q9QRH7	Q9qrh7 human immun	603	6	2.8	205	15	09WPV4	09WPV4 human immun
531	6	2.8	204	15	Q9QRH6	Q9qrh6 human immun	604	6	2.8	205	15	09WPT9	09WPT9 human immun
532	6	2.8	204	15	Q9QRH5	Q9qrh5 human immun	605	6	2.8	205	15	09Q096	09Q096 chimpanzee
533	6	2.8	204	15	Q9QRH4	Q9qrh4 human immun	606	6	2.8	205	15	09Q058	09Q058 human immun
534	6	2.8	204	15	Q9QRG0	Q9qrg0 human immun	607	6	2.8	205	15	09Q052	09Q052 human immun
535	6	2.8	204	15	Q9QRF9	Q9qrf9 human immun	608	6	2.8	205	15	09Q052	09Q052 human immun
536	6	2.8	204	15	Q9QRF8	Q9qrf8 human immun	609	6	2.8	205	15	09Q052	09Q052 human immun
537	6	2.8	204	15	Q9QRF7	Q9qrf7 human immun	610	6	2.8	205	15	09Q052	09Q052 human immun
538	6	2.8	204	15	Q9QRF6	Q9qrf6 human immun	611	6	2.8	205	15	09Q052	09Q052 human immun
539	6	2.8	204	15	Q9WPV2	Q9wpu2 human immun	612	6	2.8	205	15	09Q052	09Q052 human immun
540	6	2.8	204	15	Q9WPT4	Q9wpt4 human immun	613	6	2.8	205	15	09Q052	09Q052 human immun
541	6	2.8	204	15	Q9WP18	Q9wpl18 human immun	614	6	2.8	205	15	09Q052	09Q052 human immun
542	6	2.8	204	15	Q9Q5A6	Q9q5a6 human immun	615	6	2.8	205	15	09Q052	09Q052 human immun
543	6	2.8	204	15	Q9DQ04	Q9dqq4 human immun	616	6	2.8	205	15	09Q052	09Q052 human immun
544	6	2.8	204	15	091031	091031 human immun	617	6	2.8	205	15	09Q052	09Q052 human immun
545	6	2.8	204	15	091066	091066 human immun	618	6	2.8	205	15	09Q052	09Q052 human immun
546	6	2.8	204	15	Q72473	Q72473 human immun	619	6	2.8	205	15	09Q052	09Q052 human immun
547	6	2.8	204	15	Q99842	Q99842 human immun	620	6	2.8	205	15	09Q052	09Q052 human immun
548	6	2.8	204	15	Q74919	Q74919 human immun	621	6	2.8	205	15	09Q052	09Q052 human immun
549	6	2.8	204	15	Q74920	Q74920 human immun	622	6	2.8	205	15	09Q052	09Q052 human immun
550	6	2.8	204	15	Q74921	Q74921 human immun	623	6	2.8	205	15	09Q052	09Q052 human immun
551	6	2.8	204	15	Q75621	Q75621 human immun	624	6	2.8	205	15	09Q052	09Q052 human immun
552	6	2.8	204	15	Q75622	Q75622 human immun	625	6	2.8	205	15	09Q052	09Q052 human immun
553	6	2.8	204	15	Q75631	Q75631 human immun	626	6	2.8	205	15	09Q052	09Q052 human immun
554	6	2.8	204	15	Q75632	Q75632 human immun	627	6	2.8	205	15	09Q052	09Q052 human immun
555	6	2.8	204	15	Q75143	Q75143 human immun	628	6	2.8	205	15	09Q052	09Q052 human immun
556	6	2.8	204	15	Q75144	Q75144 human immun	629	6	2.8	205	15	09Q052	09Q052 human immun
557	6	2.8	204	15	P90266	P90266 human immun	630	6	2.8	205	15	09Q052	09Q052 human immun
558	6	2.8	204	15	Q75751	Q75751 human immun	631	6	2.8	205	15	09Q052	09Q052 human immun
559	6	2.8	204	15	Q76352	Q76352 human immun	632	6	2.8	205	15	09Q052	09Q052 human immun
560	6	2.8	204	15	Q9YNC0	Q9ync0 human immun	633	6	2.8	205	15	09Q052	09Q052 human immun
561	6	2.8	204	15	O40601	O40601 human immun	634	6	2.8	205	15	09Q052	09Q052 human immun
562	6	2.8	204	15	Q902H4	Q902h4 human immun	635	6	2.8	205	15	09Q052	09Q052 human immun
563	6	2.8	205	2	Q9S2M0	Q9s2m0 streptomyce	636	6	2.8	205	15	09Q052	09Q052 human immun
564	6	2.8	205	15	Q99586	Q99586 human immun	637	6	2.8	205	15	09Q052	09Q052 human immun
565	6	2.8	205	15	Q99623	Q99623 human immun	638	6	2.8	205	15	09Q052	09Q052 human immun
566	6	2.8	205	15	Q72436	Q72436 human immun	639	6	2.8	205	15	09Q052	09Q052 human immun
567	6	2.8	205	15	Q75713	Q75713 human immun	640	6	2.8	205	15	09Q052	09Q052 human immun
568	6	2.8	205	15	Q9W805	Q9w8u5 human immun	641	6	2.8	205	15	09Q052	09Q052 human immun
569	6	2.8	205	15	Q9PX72	Q9px72 human immun	642	6	2.8	205	15	09Q052	09Q052 human immun
570	6	2.8	205	15	Q9PX02	Q9px02 human immun	643	6	2.8	205	15	09Q052	09Q052 human immun
571	6	2.8	205	15	Q9PW28	Q9pwz8 human immun	644	6	2.8	205	15	09Q052	09Q052 human immun
572	6	2.8	205	15	Q40592	Q40592 human immun	645	6	2.8	205	15	09Q052	09Q052 human immun
573	6	2.8	205	15	Q9DGUI	Q9dgui human immun	646	6	2.8	205	15	09Q052	09Q052 human immun
574	6	2.8	205	15	Q9QNF1	Q9qnf1 human immun	647	6	2.8	205	15	09Q052	09Q052 human immun
575	6	2.8	205	15	Q9QNF0	Q9qnf0 human immun	648	6	2.8	205	15	09Q052	09Q052 human immun
576	6	2.8	205	15	Q9QNE9	Q9qne9 human immun	649	6	2.8	205	15	09Q052	09Q052 human immun
577	6	2.8	205	15	Q9QNE8	Q9qne8 human immun	650	6	2.8	205	15	09Q052	09Q052 human immun
578	6	2.8	205	15	Q9QNE6	Q9qne6 human immun	651	6	2.8	205	15	09Q052	09Q052 human immun
579	6	2.8	205	15	Q9QNE5	Q9qne5 human immun	652	6	2.8	205	15	09Q052	09Q052 human immun
580	6	2.8	205	15	Q9QNE3	Q9qne3 human immun	653	6	2.8	205	15	09Q052	09Q052 human immun
581	6	2.8	205	15	Q9QND8	Q9qnd8 human immun	654	6	2.8	205	15	09Q052	09Q052 human immun
582	6	2.8	205	15	Q9WLX6	Q9wlx6 human immun	655	6	2.8	205	15	09Q052	09Q052 human immun
583	6	2.8	205	15	Q9WLX5	Q9wlx5 human immun	656	6	2.8	205	15	09Q052	09Q052 human immun
584	6	2.8	205	15	Q71126	Q71126 human immun	657	6	2.8	205	15	09Q052	09Q052 human immun
585	6	2.8	205	15	Q9YX71	Q9yx71 human immun	658	6	2.8	205	15	09Q052	09Q052 human immun
586	6	2.8	205	15	Q72628	Q72628 human immun	659	6	2.8	205	15	09Q052	09Q052 human immun
587	6	2.8	205	15	Q72631	Q72631 human immun	660	6	2.8	205	15	09Q052	09Q052 human immun
588	6	2.8	205	15	Q9QSQ6	Q9qsg6 human immun	661	6	2.8	205	15	09Q052	09Q052 human immun
589	6	2.8	205	15	Q90500	Q90500 human immun	662	6	2.8	205	15	09Q052	09Q052 human immun
590	6	2.8	205	15	Q90509	Q90509 human immun	663	6	2.8	205	15	09Q052	09Q052 human immun
591	6	2.8	205	15	Q90521	Q90521 human immun	664	6	2.8	205	15	09Q052	09Q052 human immun
592	6	2.8	205	15	Q90522	Q90522 human immun	665	6	2.8	205	15	09Q052	09Q052 human immun
593	6	2.8	205	15	Q90528	Q90528 human immun	666	6	2.8	205	15	09Q052	09Q052 human immun
594	6	2.8	205	15	Q90645	Q90645 human immun	667	6	2.8	205	15	09Q052	09Q052 human immun
595	6	2.8	205	15	Q9QRJ0	Q9qrj0 human immun	668	6	2.8	205	15	09Q052	09Q052 human immun
596	6	2.8	205	15	Q9QRJ7	Q9qrj7 human immun	669	6	2.8	205	15	09Q052	09Q052 human immun
597	6	2.8	205	15	Q9WPX8	Q9wpx8 human immun	670	6	2.8	205	15	09Q052	09Q052 human immun
598	6	2.8	205	15	Q9WPW2	Q9wpw2 human immun	671	6	2.8	205	15	09Q052	09Q052 human immun
599	6	2.8	205	15	Q9WPV9	Q9wpv9 human immun	672	6	2.8	205	15	09Q052	09Q052 human immun
600	6	2.8	205	15			673	6	2.8	205	15	09Q052	09Q052 human immun

674	6	2.8	205	15	Q75714	Q75714 human	747	6	2.8	206	15	Q9PWW0	Q9PWW0 human
675	6	2.8	205	15	Q75715	Q75715 human	748	6	2.8	206	15	Q9PWT7	Q9PWT7 human
676	6	2.8	205	15	Q75716	Q75716 human	749	6	2.8	206	15	Q9WA35	Q9WA35 human
677	6	2.8	205	15	Q75717	Q75717 human	750	6	2.8	206	15	Q9IR09	Q9IR09 human
678	6	2.8	205	15	P88405	P88405 human	751	6	2.8	206	15	Q9IR08	Q9IR08 human
679	6	2.8	205	15	P88407	P88407 human	752	6	2.8	206	15	Q9IR07	Q9IR07 human
680	6	2.8	205	15	P88408	P88408 human	753	6	2.8	206	15	Q9IR06	Q9IR06 human
681	6	2.8	205	15	P88409	P88409 human	754	6	2.8	206	15	Q9IR05	Q9IR05 human
682	6	2.8	205	15	P88410	P88410 human	755	6	2.8	206	15	Q9IQ29	Q9IQ29 human
683	6	2.8	205	15	P88411	P88411 human	756	6	2.8	206	15	Q9IQ28	Q9IQ28 human
684	6	2.8	205	15	P88412	P88412 human	757	6	2.8	206	15	Q9IQ26	Q9IQ26 human
685	6	2.8	205	15	P88413	P88413 human	758	6	2.8	206	15	Q9IQ25	Q9IQ25 human
686	6	2.8	205	15	P88414	P88414 human	759	6	2.8	206	15	Q9IQ24	Q9IQ24 human
687	6	2.8	205	15	P88415	P88415 human	760	6	2.8	206	15	Q9IQ23	Q9IQ23 human
688	6	2.8	205	15	P88416	P88416 human	761	6	2.8	206	15	Q9IQ21	Q9IQ21 human
689	6	2.8	205	15	P88417	P88417 human	762	6	2.8	206	15	Q40177	Q40177 human
690	6	2.8	205	15	P88418	P88418 human	763	6	2.8	206	15	Q40178	Q40178 human
691	6	2.8	205	15	P88420	P88420 human	764	6	2.8	206	15	Q40223	Q40223 human
692	6	2.8	205	15	P88421	P88421 human	765	6	2.8	206	15	Q70896	Q70896 human
693	6	2.8	205	15	P88422	P88422 human	766	6	2.8	206	15	Q9WM29	Q9WM29 human
694	6	2.8	205	15	P88423	P88423 human	767	6	2.8	206	15	Q9WM28	Q9WM28 human
695	6	2.8	205	15	P88424	P88424 human	768	6	2.8	206	15	Q9WM24	Q9WM24 human
696	6	2.8	205	15	P88425	P88425 human	769	6	2.8	206	15	Q9WM23	Q9WM23 human
697	6	2.8	205	15	P88427	P88427 human	770	6	2.8	206	15	Q9WM17	Q9WM17 human
698	6	2.8	205	15	P88428	P88428 human	771	6	2.8	206	15	Q9WM16	Q9WM16 human
699	6	2.8	205	15	P88429	P88429 human	772	6	2.8	206	15	Q92771	Q92771 human
700	6	2.8	205	15	P88430	P88430 human	773	6	2.8	206	15	Q9WIX9	Q9WIX9 human
701	6	2.8	205	15	Q76349	Q76349 human	774	6	2.8	206	15	Q9WIX8	Q9WIX8 human
702	6	2.8	205	15	Q76350	Q76350 human	775	6	2.8	206	15	Q71085	Q71085 human
703	6	2.8	205	15	Q40591	Q40591 human	776	6	2.8	206	15	Q9WIX7	Q9WIX7 human
704	6	2.8	205	15	Q90MK4	Q90MK4 human	777	6	2.8	206	15	Q71086	Q71086 human
705	6	2.8	205	15	Q908M1	Q908M1 human	778	6	2.8	206	15	Q9WIX4	Q9WIX4 human
706	6	2.8	205	15	Q908K3	Q908K3 human	779	6	2.8	206	15	Q9WIX3	Q9WIX3 human
707	6	2.8	205	15	Q908J4	Q908J4 human	780	6	2.8	206	15	Q92772	Q92772 human
708	6	2.8	205	15	Q908I5	Q908I5 human	781	6	2.8	206	15	Q9WIX2	Q9WIX2 human
709	6	2.8	205	15	Q902U1	Q902U1 human	782	6	2.8	206	15	Q9WIX1	Q9WIX1 human
710	6	2.8	205	15	Q902S3	Q902S3 human	783	6	2.8	206	15	Q9WIX0	Q9WIX0 human
711	6	2.8	205	15	Q902P6	Q902P6 human	784	6	2.8	206	15	Q71087	Q71087 human
712	6	2.8	205	15	Q902N7	Q902N7 human	785	6	2.8	206	15	Q9WIX9	Q9WIX9 human
713	6	2.8	205	15	Q902G5	Q902G5 human	786	6	2.8	206	15	Q92887	Q92887 human
714	6	2.8	206	12	Q92094	Q92094 tobacco	787	6	2.8	206	15	Q9WIM7	Q9WIM7 human
715	6	2.8	206	13	Q9YGD8	Q9YGD8 oncorhynch	788	6	2.8	206	15	Q9WIM6	Q9WIM6 human
716	6	2.8	206	15	Q9S561	Q9S561 human	789	6	2.8	206	15	Q9WIM5	Q9WIM5 human
717	6	2.8	206	15	Q9S766	Q9S766 human	790	6	2.8	206	15	Q9WIM4	Q9WIM4 human
718	6	2.8	206	15	Q9S966	Q9S966 human	791	6	2.8	206	15	Q92938	Q92938 human
719	6	2.8	206	15	Q9S553	Q9S553 human	792	6	2.8	206	15	Q9WIL6	Q9WIL6 human
720	6	2.8	206	15	Q9S980	Q9S980 human	793	6	2.8	206	15	Q72621	Q72621 human
721	6	2.8	206	15	Q9A430	Q9A430 human	794	6	2.8	206	15	Q72623	Q72623 human
722	6	2.8	206	15	Q9A436	Q9A436 human	795	6	2.8	206	15	Q72625	Q72625 human
723	6	2.8	206	15	Q9S511	Q9S511 human	796	6	2.8	206	15	Q72626	Q72626 human
724	6	2.8	206	15	Q9S515	Q9S515 human	797	6	2.8	206	15	Q72629	Q72629 human
725	6	2.8	206	15	Q9S537	Q9S537 human	798	6	2.8	206	15	Q93010	Q93010 human
726	6	2.8	206	15	Q9S575	Q9S575 human	799	6	2.8	206	15	Q72632	Q72632 human
727	6	2.8	206	15	Q9S587	Q9S587 human	800	6	2.8	206	15	Q72635	Q72635 human
728	6	2.8	206	15	Q9S630	Q9S630 human	801	6	2.8	206	15	Q72636	Q72636 human
729	6	2.8	206	15	Q9S668	Q9S668 human	802	6	2.8	206	15	Q72647	Q72647 human
730	6	2.8	206	15	Q9S688	Q9S688 human	803	6	2.8	206	15	Q72648	Q72648 human
731	6	2.8	206	15	Q9S706	Q9S706 human	804	6	2.8	206	15	Q72649	Q72649 human
732	6	2.8	206	15	Q9S778	Q9S778 human	805	6	2.8	206	15	Q72650	Q72650 human
733	6	2.8	206	15	Q9S851	Q9S851 human	806	6	2.8	206	15	Q72651	Q72651 human
734	6	2.8	206	15	Q9S888	Q9S888 human	807	6	2.8	206	15	Q72652	Q72652 human
735	6	2.8	206	15	Q9S889	Q9S889 human	808	6	2.8	206	15	Q93012	Q93012 human
736	6	2.8	206	15	O12390	O12390 human	809	6	2.8	206	15	Q9W7X3	Q9W7X3 human
737	6	2.8	206	15	O12404	O12404 human	810	6	2.8	206	15	Q9W7X2	Q9W7X2 human
738	6	2.8	206	15	Q9S629	Q9S629 human	811	6	2.8	206	15	Q93013	Q93013 human
739	6	2.8	206	15	Q9YJ66	Q9YJ66 human	812	6	2.8	206	15	Q93014	Q93014 human
740	6	2.8	206	15	Q75752	Q75752 human	813	6	2.8	206	15	Q9W7X1	Q9W7X1 human
741	6	2.8	206	15	Q75718	Q75718 human	814	6	2.8	206	15	Q9W7X0	Q9W7X0 human
742	6	2.8	206	15	Q9W9N0	Q9W9N0 human	815	6	2.8	206	15	Q90179	Q90179 human
743	6	2.8	206	15	Q9W7U0	Q9W7U0 human	816	6	2.8	206	15	Q9QSU1	Q9QSU1 human
744	6	2.8	206	15	Q9PWX9	Q9PWX9 human	817	6	2.8	206	15	Q90502	Q90502 human
745	6	2.8	206	15	Q9PWX8	Q9PWX8 human	818	6	2.8	206	15	Q90505	Q90505 human
746	6	2.8	206	15	Q9PXX7	Q9PXX7 human	819	6	2.8	206	15	Q90511	Q90511 human

820	6	2.8	206	15	090526	090526	human	immun	893	6	2.8	206	15	090526	090526	human	immun
821	6	2.8	206	15	090644	090644	human	immun	894	6	2.8	206	15	0905d5	0905d5	human	immun
822	6	2.8	206	15	090RX0	090RX0	human	immun	895	6	2.8	206	15	0905d5	0905d5	human	immun
823	6	2.8	206	15	090RL1	090RL1	human	immun	896	6	2.8	206	15	0905d3	0905d3	human	immun
824	6	2.8	206	15	090RL0	090RL0	human	immun	897	6	2.8	206	15	0905d2	0905d2	human	immun
825	6	2.8	206	15	090RK9	090RK9	human	immun	898	6	2.8	206	15	0905B9	0905B9	human	immun
826	6	2.8	206	15	090RK8	090RK8	human	immun	899	6	2.8	206	15	0905B8	0905B8	human	immun
827	6	2.8	206	15	090RK7	090RK7	human	immun	900	6	2.8	206	15	0905B1	0905B1	human	immun
828	6	2.8	206	15	090RK6	090RK6	human	immun	901	6	2.8	206	15	0905B0	0905B0	human	immun
829	6	2.8	206	15	090RK5	090RK5	human	immun	902	6	2.8	206	15	0905A8	0905A8	human	immun
830	6	2.8	206	15	090RK4	090RK4	human	immun	903	6	2.8	206	15	0905A7	0905A7	human	immun
831	6	2.8	206	15	090RK3	090RK3	human	immun	904	6	2.8	206	15	0905A3	0905A3	human	immun
832	6	2.8	206	15	090RK2	090RK2	human	immun	905	6	2.8	206	15	090599	090599	human	immun
833	6	2.8	206	15	090RK1	090RK1	human	immun	906	6	2.8	206	15	090598	090598	human	immun
834	6	2.8	206	15	090RJ2	090RJ2	human	immun	907	6	2.8	206	15	090597	090597	human	immun
835	6	2.8	206	15	090RJ1	090RJ1	human	immun	908	6	2.8	206	15	090596	090596	human	immun
836	6	2.8	206	15	090RI4	090RI4	human	immun	909	6	2.8	206	15	090595	090595	human	immun
837	6	2.8	206	15	090RI3	090RI3	human	immun	910	6	2.8	206	15	090594	090594	human	immun
838	6	2.8	206	15	090RI2	090RI2	human	immun	911	6	2.8	206	15	090RW3	090RW3	human	immun
839	6	2.8	206	15	090RI1	090RI1	human	immun	912	6	2.8	206	15	090RW2	090RW2	human	immun
840	6	2.8	206	15	090RI0	090RI0	human	immun	913	6	2.8	206	15	090RW1	090RW1	human	immun
841	6	2.8	206	15	090RH9	090RH9	human	immun	914	6	2.8	206	15	090RW0	090RW0	human	immun
842	6	2.8	206	15	090RH8	090RH8	human	immun	915	6	2.8	206	15	090RV9	090RV9	human	immun
843	6	2.8	206	15	090RF5	090RF5	human	immun	916	6	2.8	206	15	090RV8	090RV8	human	immun
844	6	2.8	206	15	090RF4	090RF4	human	immun	917	6	2.8	206	15	090RV7	090RV7	human	immun
845	6	2.8	206	15	090RF3	090RF3	human	immun	918	6	2.8	206	15	090RV6	090RV6	human	immun
846	6	2.8	206	15	090RF2	090RF2	human	immun	919	6	2.8	206	15	090RV5	090RV5	human	immun
847	6	2.8	206	15	090RF1	090RF1	human	immun	920	6	2.8	206	15	090RV4	090RV4	human	immun
848	6	2.8	206	15	090RF0	090RF0	human	immun	921	6	2.8	206	15	090RU6	090RU6	human	immun
849	6	2.8	206	15	090RE9	090RE9	human	immun	922	6	2.8	206	15	090RU5	090RU5	human	immun
850	6	2.8	206	15	090RE8	090RE8	human	immun	923	6	2.8	206	15	090RU2	090RU2	human	immun
851	6	2.8	206	15	090RD9	090RD9	human	immun	924	6	2.8	206	15	090RS9	090RS9	human	immun
852	6	2.8	206	15	090RD8	090RD8	human	immun	925	6	2.8	206	15	090RS4	090RS4	human	immun
853	6	2.8	206	15	090RD7	090RD7	human	immun	926	6	2.8	206	15	090RS3	090RS3	human	immun
854	6	2.8	206	15	090RD5	090RD5	human	immun	927	6	2.8	206	15	090RS2	090RS2	human	immun
855	6	2.8	206	15	090PY2	090PY2	human	immun	928	6	2.8	206	15	090RS1	090RS1	human	immun
856	6	2.8	206	15	090PY1	090PY1	human	immun	929	6	2.8	206	15	090RG9	090RG9	human	immun
857	6	2.8	206	15	090WPX7	090WPX7	human	immun	930	6	2.8	206	15	09JOG4	09JOG4	human	immun
858	6	2.8	206	15	090WPX3	090WPX3	human	immun	931	6	2.8	206	15	09IH71	09IH71	human	immun
859	6	2.8	206	15	090WPX2	090WPX2	human	immun	932	6	2.8	206	15	09IH69	09IH69	human	immun
860	6	2.8	206	15	090WPX0	090WPX0	human	immun	933	6	2.8	206	15	09IH68	09IH68	human	immun
861	6	2.8	206	15	090WPW9	090WPW9	human	immun	934	6	2.8	206	15	09IH67	09IH67	human	immun
862	6	2.8	206	15	090WPW6	090WPW6	human	immun	935	6	2.8	206	15	09IH65	09IH65	human	immun
863	6	2.8	206	15	090WPW4	090WPW4	human	immun	936	6	2.8	206	15	09IH64	09IH64	human	immun
864	6	2.8	206	15	090WPW0	090WPW0	human	immun	937	6	2.8	206	15	09DQJ1	09DQJ1	human	immun
865	6	2.8	206	15	090WPV8	090WPV8	human	immun	938	6	2.8	206	15	09DQT9	09DQT9	human	immun
866	6	2.8	206	15	090WPV7	090WPV7	human	immun	939	6	2.8	206	15	09DQT6	09DQT6	human	immun
867	6	2.8	206	15	090WPV4	090WPV4	human	immun	940	6	2.8	206	15	09DQT5	09DQT5	human	immun
868	6	2.8	206	15	090WPV9	090WPV9	human	immun	941	6	2.8	206	15	09DQJ3	09DQJ3	human	immun
869	6	2.8	206	15	090WPJ7	090WPJ7	human	immun	942	6	2.8	206	15	09DQJ2	09DQJ2	human	immun
870	6	2.8	206	15	090WPJ3	090WPJ3	human	immun	943	6	2.8	206	15	09DQJ1	09DQJ1	human	immun
871	6	2.8	206	15	090WPJ0	090WPJ0	human	immun	944	6	2.8	206	15	09DQJ0	09DQJ0	human	immun
872	6	2.8	206	15	090WPT5	090WPT5	human	immun	945	6	2.8	206	15	09DQF8	09DQF8	human	immun
873	6	2.8	206	15	090WPS9	090WPS9	human	immun	946	6	2.8	206	15	09DQP7	09DQP7	human	immun
874	6	2.8	206	15	090WPJ7	090WPJ7	human	immun	947	6	2.8	206	15	09DQP6	09DQP6	human	immun
875	6	2.8	206	15	090WPJ6	090WPJ6	human	immun	948	6	2.8	206	15	09DQP5	09DQP5	human	immun
876	6	2.8	206	15	090WPJ4	090WPJ4	human	immun	949	6	2.8	206	15	09DQP4	09DQP4	human	immun
877	6	2.8	206	15	090WPJ1	090WPJ1	human	immun	950	6	2.8	206	15	09DQP3	09DQP3	human	immun
878	6	2.8	206	15	090WPF2	090WPF2	human	immun	951	6	2.8	206	15	09E2H7	09E2H7	human	immun
879	6	2.8	206	15	09QJ080	09QJ080	chimpanzee		952	6	2.8	206	15	0994Q5	0994Q5	human	immun
880	6	2.8	206	15	09Q6W8	09Q6W8	human	immun	953	6	2.8	206	15	0994N7	0994N7	human	immun
881	6	2.8	206	15	09Q5H6	09Q5H6	human	immun	954	6	2.8	206	15	0994L0	0994L0	human	immun
882	6	2.8	206	15	09Q5H5	09Q5H5	human	immun	955	6	2.8	206	15	0994K1	0994K1	human	immun
883	6	2.8	206	15	09Q5H4	09Q5H4	human	immun	956	6	2.8	206	15	0994J6	0994J6	human	immun
884	6	2.8	206	15	09Q5H3	09Q5H3	human	immun	957	6	2.8	206	15	0930Z5	0930Z5	human	immun
885	6	2.8	206	15	09Q5F8	09Q5F8	human	immun	958	6	2.8	206	15	0910L0	0910L0	human	immun
886	6	2.8	206	15	09Q5F7	09Q5F7	human	immun	959	6	2.8	206	15	0910Z5	0910Z5	human	immun
887	6	2.8	206	15	09Q5F2	09Q5F2	human	immun	960	6	2.8	206	15	0910S3	0910S3	human	immun
888	6	2.8	206	15	09Q5F1	09Q5F1	human	immun	961	6	2.8	206	15	09WK41	09WK41	human	immun
889	6	2.8	206	15	09Q5F0	09Q5F0	human	immun	962	6	2.8	206	15	09WK40	09WK40	human	immun
890	6	2.8	206	15	09Q5E9	09Q5E9	human	immun	963	6	2.8	206	15	0910Z4	0910Z4	human	immun
891	6	2.8	206	15	09Q5E8	09Q5E8	human	immun	964	6	2.8	206	15	0910Z3	0910Z3	human	immun
892	6	2.8	206	15	09Q5E7	09Q5E7	human	immun	965	6	2.8	206	15	0910Z6	0910Z6	human	immun

966 6 2.8 206 15 O91059 human immun
967 6 2.8 206 15 O91061 human immun
968 6 2.8 206 15 O9WK39 human immun
969 6 2.8 206 15 O91062 human immun
970 6 2.8 206 15 O9WK38 human immun
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972 6 2.8 206 15 O91073 human immun
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974 6 2.8 206 15 O91075 human immun
975 6 2.8 206 15 O9DKF7 human immun
976 6 2.8 206 15 O9DKF9 human immun
977 6 2.8 206 15 O9DKF1 human immun
978 6 2.8 206 15 O9783 human immun
979 6 2.8 206 15 O9782 human immun
980 6 2.8 206 15 O97673 human immun
981 6 2.8 206 15 O97674 human immun
982 6 2.8 206 15 O97675 human immun
983 6 2.8 206 15 O97676 human immun
984 6 2.8 206 15 O97677 human immun
985 6 2.8 206 15 O97678 human immun
986 6 2.8 206 15 O97680 human immun
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994 6 2.8 206 15 O97691 human immun
995 6 2.8 206 15 O97692 human immun
996 6 2.8 206 15 O97693 human immun
997 6 2.8 206 15 O97694 human immun
998 6 2.8 206 15 O97695 human immun
999 6 2.8 206 15 O97696 human immun
1000 6 2.8 206 15 O97697 human immun

ALIGNMENTS

RESULT 1
Q9EST9 ID Q9EST9 PRELIMINARY; PRT; 212 AA.
AC Q9EST9; 2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE FGF-20.
GN FGF-20.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADULT BRAIN.
RX MEDLINE=20490008; PubMed=11032730;
RA Ohmachi S., Watanabe Y., Mikami T., Kusu N., Ibi T., Akaike A.,
RA Itoh N.;
RA "FGF-20, a novel neurotrophic factor, preferentially expressed in the
RT substantia nigra pars compacta of rat brain."
RL Biochem. Biophys. Res. Commun. 277:355-360(2000).
DR EMBL; AB020021; BAB13763.1; -.
DR HSSP; P31371; 1G82.
DR InterPro; IPR002209; HBGFG_FGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; HBGFG_FGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGFG_FGF; 1.
SQ SEQUENCE 212 AA; 29537 MW; 4F858B8E7F72B977 CRC64;

Query Match 40.3%; Score 85; DB 11; Length 212;
Best Local Similarity 100.0%; Pred. No. 9.2e-79;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 124 KGLYSGSEKLTSECIFRQFEENWYNTYSSNIYKHGDTGRYFVALNKDCTPRDGARSKR 183
DB 124 KGLYSGSEKLTSECIFRQFEENWYNTYSSNIYKHGDTGRYFVALNKDCTPRDGARSKR 183
QY 184 HQKTHFLPRVDPVPELYKDLL 208
DB 184 HQKTHFLPRVDPVPELYKDLL 208
RESULT 2
Q9ESL9 ID Q9ESL9 PRELIMINARY; PRT; 212 AA.
AC Q9ESL9; 2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE FIBROBLAST GROWTH FACTOR 20.
GN FGF20.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A.
RA Itoh N.;
RT "Mus musculus mRNA for FGF-20(FGF20).";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049218; BAB16406.1; -.
DR HSSP; P31371; 1G82.
DR MGD; MGI:1891346; Fgf20.
DR InterPro; IPR002209; HBGFG_FGF.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; HBGFG_FGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGFG_FGF; 1.
SQ SEQUENCE 212 AA; 23659 MW; 174DBCE8915B69EF CRC64;
Query Match 35.5%; Score 75; DB 11; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.6e-68;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 85 VQGTQDHSLSGLFISVAVGLVSGVDSGLYGMNDKGLYSGSEKLTSECIFRQFE 144
DB 85 VQGTQDHSLSGLFISVAVGLVSGVDSGLYGMNDKGLYSGSEKLTSECIFRQFE 144
QY 145 ENWYNTYSSNIYKHG 159
DB 145 ENWYNTYSSNIYKHG 159
RESULT 3
Q9PVY1 ID Q9PVY1 PRELIMINARY; PRT; 208 AA.
AC Q9PVY1; 2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE XFGF-20.
GN XFGF-20.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
ON NCBI_TaxID=8355;
RX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99373151; PubMed=10441498;


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RA Koga C., Adati N., Nakata K., Mikoshiba K., Furuhata Y., Sato S.,
RA Tei H., Sakaki Y., Kurokawa T., Shiohara K., Yokoyama K.K.:
RT "Characterization of a novel member of the FGF family, XFGF-20, in
RL Xenopus laevis."; Res. Commun. 261:756-765(1999).
DR EMBL; AB012615; BAA83474.1; -.
DR HSSP; P31371; IG82.
DR InterPro; IPR002209; HBGFG_FGF.
DR DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; ILI_HBGF.
DR PRODOM; PD000831; HBGFG_FGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGFG_FGF; 1.
SQ SEQUENCE 208 AA; 23438 MW; 269881D36E757D4D CRC64;

Query Match 12.3%; Score 26; DB 13; Length 208;
Best Local Similarity 100.0%; Pred. No. 2.5e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 GSEKLTSECFRQFEENWNTYSSN 154
DB 126 GSEKLTSECFRQFEENWNTYSSN 151
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RESULT 4
Q95L12 PRELIMINARY; PRT; 208 AA.
AC Q95L12;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE FTBROBLAST GROWTH FACTOR 9.
GN FGF9.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Paradis V., Silversides D.W.;
RT "Sus scrofa fgf9 cDNA.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY033825; AAK61609.2; -.
SQ SEQUENCE 208 AA; 23454 MW; 05FD0E2048CC5E5 CRC64;

Query Match 9.0%; Score 19; DB 6; Length 208;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVSRGVDSGLYLGMN 122
DB 101 AVGLVSRGVDSGLYLGMN 119
|||||
RESULT 5
Q9ESL8 PRELIMINARY; PRT; 207 AA.
AC Q9ESL8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE FTBROBLAST GROWTH FACTOR 16.
GN FGF16.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Itoh N.;
RT "Mus musculus mRNA for FGF-16 (FGF16).";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AB049219; BAB16405.1; -.
DR HSSP; P31371; IG82.
DR MGD; MGI:1931627; Fgf16.
DR InterPro; IPR002209; HBGFG_FGF.
DR DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; ILI_HBGF.
DR PRODOM; PD000831; HBGFG_FGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGFG_FGF; 1.
SQ SEQUENCE 207 AA; 23751 MW; 68BD03EBDAAD1D84E CRC64;

Query Match 7.6%; Score 16; DB 11; Length 207;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 GILRRRLYCRGTGFHL 77
DB 58 GILRRRLYCRGTGFHL 73
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RESULT 6
Q9ERQ5 PRELIMINARY; PRT; 207 AA.
AC Q9ERQ5;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE FGF-16 PROTEIN.
GN FGF16.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Sontag D.P., Cattini P.A.;
RT "Cloning and biological function of FGF-16 in the heart.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF292104; AAG29501.1; -.
DR HSSP; P31371; IG82.
DR MGD; MGI:1931627; Fgf16.
DR InterPro; IPR002209; HBGFG_FGF.
DR DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; ILI_HBGF.
DR PRODOM; PD000831; HBGFG_FGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGFG_FGF; 1.
SQ SEQUENCE 207 AA; 23739 MW; E28004DED598A2C6 CRC64;

Query Match 7.6%; Score 16; DB 11; Length 207;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 GILRRRLYCRGTGFHL 77
DB 58 GILRRRLYCRGTGFHL 73
|||||
RESULT 7
Q9S9P9 PRELIMINARY; PRT; 197 AA.
AC Q9S9P9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE F26G16.12 PROTEIN.
GN F26G16.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

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OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
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RN SEQUENCE FROM N.A.
RP STRAIN=CV. COLUMBIA;
RA Liu S.X., Sakano H., Yu G., Jhaveri A., Lee J.M., Lenz C., Pham P.,
RA Toriumi M., Chin C., Chlou J., Choi E., Chung M., Gonzalez A.,
RA Hwang B., Koo T., Li J., Liu A., Vaysberg M., Altafi H., Brooks S.,
RA Buehler E., Chao Q., Conn L., Conway A., Hansen N., Johnson-Hopson C.,
RA Khan S., Kim C., Lam B., Nguyen M., Palm C., Shinn P., Tambunga G.,
RA Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
RT "Arabidopsis thaliana chromosome 1 BAC F26G16 sequence.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=CV. COLUMBIA;
RA Theologis A.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC009917; AAF19754.1; -.
DR InterPro; IPR001289; CBF_NFYA.
DR Pfam; PF02045; CBF_NFYA; 1.
DR PRINTS; PR00616; CCAATSUBUNT.
DR PRODOM; PD003860; CBF_NFYA; 1.
DR SMART; SM00521; CBF; 1.
SQ SEQUENCE 197 AA; 22127 MW; EB67C5050BE0F874 CRC64;

Query Match          3.8%; Score 8; DB 10; Length 197;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 HGILRRRQ 68
DB 117 HGILRRRQ 124

RESULT 8
Q9M607 PRELIMINARY; PRT; 215 AA.
ID Q9M607
AC Q9M607
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
DE TRANSCRIPTION FACTOR.
GN REV136-2.
OS Vitis riparia (Frost grape) (Vitis vulpina).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae;
OC Vitis.
OX NCBI_TaxID=96939;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=FLOWER BUDS;
RA Li X.Z., McKersie B.D.;
RT "Freezing tolerance in grapevines.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220405; AAF37266.1; -.
DR InterPro; IPR001289; CBF_NFYA.
DR Pfam; PF02045; CBF_NFYA; 1.
DR PRINTS; PR00616; CCAATSUBUNT.
DR PRODOM; PD003860; CBF_NFYA; 1.
DR SMART; SM00521; CBF; 1.
SQ SEQUENCE 215 AA; 24311 MW; EBCB7BB5921E415E CRC64;

Query Match          3.8%; Score 8; DB 10; Length 215;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 HGILRRRQ 68
DB 56 HGILRRRQ 63

RESULT 9
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O64585 PRELIMINARY; PRT; 226 AA.
ID O64585
AC O64585
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE PUTATIVE CCAAT-BOX-BINDING TRANSCRIPTION FACTOR SUBUNIT.
GN AT2G34720.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=CV. COLUMBIA;
RA MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.";
RL Nature 402:761-768(1999).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC003096; AAC16262.1; -.
DR InterPro; IPR001289; CBF_NFYA.
DR Pfam; PF02045; CBF_NFYA; 1.
DR PRINTS; PR00616; CCAATSUBUNT.
DR PRODOM; PD003860; CBF_NFYA; 1.
DR SMART; SM00521; CBF; 1.
SQ SEQUENCE 226 AA; 25786 MW; 35047340C2202018 CRC64;

Query Match          3.8%; Score 8; DB 10; Length 226;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 HGILRRRQ 68
DB 136 HGILRRRQ 143

RESULT 10
O70128 PRELIMINARY; PRT; 275 AA.
ID O70128
AC O70128
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE PUTATIVE AIPASE (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=98217376; PubMed=9548971;
RA Halleck M.S., Pradhan D., Blackman C., Berkes C., Williamson P.,
RA Schlegel R.A.;
RT "Multiple members of a third subfamily of P-type ATPases identified by genomic sequences and ESTs.";
RL Genome Res. 8:354-361(1998).
DR EMBL; U78977; AAC05244.1; -.
DR InterPro; IPR000150; Hypothet_cof.
DR NON_TER 1
FT SEQUENCE 275 AA; 31000 MW; 067CF9B1FB0A5879 CRC64;
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Query Match          3.8%; Score 8; DB 11; Length 275;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 PELYKDLL 208
DB 135 PELYKDLL 142

RESULT 11
Q9M332 ID Q9M332 PRELIMINARY; PRT; 545 AA.
AC Q9M332;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 60.0 KDA PROTEIN (AT3G53950/F5K20_250).
GN F5K20_250.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Monfort A., Casacuberta E., Puigdomenech P., Mewes H.W., Rudd S.,
RA Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RA Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RA Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
RA Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RA "Arabidopsis cDNA clones."
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AL132960; CAB88357.1; -.
DR EMBL; AY054205; AAL08666.1; -.
KW Hypothetical protein.
SQ SEQUENCE 545 AA; 60004 MW; 14745A770BBB53C5 CRC64;

Query Match          3.8%; Score 8; DB 10; Length 545;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 QILPDGSV 85
DB 172 QILPDGSV 179

RESULT 12
Q9X2Y5 ID Q9X2Y5 PRELIMINARY; PRT; 564 AA.
AC Q9X2Y5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PX01-14.
OS Bacillus anthracis.
OG Plasmid virulence plasmid pX01.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1392;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=STERNE;
RX MEDLINE=99445483; PubMed=10515943;
RA Okinaka R.T., Cloud K., Hampton O., Hoffmaster A.R., Hill K.K.,
RA Kelm P., Koehler T.M., Lamke G., Kumano S., Mahillon J., Manter D.,
RA Martinez Y., Ricke D., Svensson R., Jackson P.J.;
RT "Sequence and organization of pX01, the large Bacillus anthracis
RT plasmid harboring the anthrax toxin genes.";
RL J. Bacteriol. 181:6509-6515(1999).
DR EMBL; AF065404; AAD32318.1; -.
KW Plasmid.
SQ SEQUENCE 564 AA; 66521 MW; D22C87DBA68DF021 CRC64;

Query Match          3.8%; Score 8; DB 2; Length 564;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 LYGSEKLT 134
DB 329 LYGSEKLT 336

RESULT 13
Q922L9 ID Q922L9 PRELIMINARY; PRT; 964 AA.
AC Q922L9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO ATPASE, CLASS II, TYPE 9A (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006949; AAH06949.1; -.
FT NON_TER
SQ SEQUENCE 964 AA; 108661 MW; 377DEDA4D53BEC27 CRC64;

Query Match          3.8%; Score 8; DB 11; Length 964;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 PELYKDLL 208
DB 824 PELYKDLL 831

RESULT 14
Q9KCW8 ID Q9KCW8 PRELIMINARY; PRT; 70 AA.
AC Q9KCW8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE BHI451 PROTEIN.
GN BHI451.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C-125 / JCM 9153;
RC MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hiram C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";

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RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL; AP001512; BAB05170.1; -.
 KW Complete proteome.
 SQ SEQUENCE 70 AA; 8093 MW; 53DCBAB438D7262A CRC64;
 Query Match 3.3%; Score 7; DB 16; Length 70;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 GGFLGGL 14
 |||||
 DB 34 GGFLGGL 40

RESULT 15

Q9PE80
 ID Q9PE80 PRELIMINARY; PRT: 101 AA.
 AC Q9PE80;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ATP SYNTHASE C CHAIN (EC 3.6.1.34) (LIPID-BINDING PROTEIN) (SUBUNIT C).
 DE C).
 GN XF1148.
 OS Xylella fastidiosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC Xylella.
 OX NCBI_TaxID=2371;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=9A5C;
 RX MEDLINE=20365717; PubMed=10910347;
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
 RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
 RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
 RL Nature 406:151-159(2000).
 CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
 CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
 CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
 CC HAS THREE MAIN SUBUNITS: A, B AND C (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ATPASE C CHAIN FAMILY.
 CC EMBL: AC003950; AAF83958.1; -.
 DR HSSP: P00844; 1A91.
 DR InterPro: IPR002379; ATPase_C.
 DR InterPro: IPR000454; ATPase_C_eub.
 DR Pfam: PF00137; ATP-synt.C; 1.
 DR PRINTS: PR00124; ATPASEC.
 DR PROSITE: PS00605; ATPASE_C; 1.
 KW CF(0): Complete proteome; Hydrogen ion transport; Lipid-binding;

KW Transmembrane.
 SQ SEQUENCE 101 AA; 10255 MW; 7017ADA5B34C69F0 CRC64;
 Query Match 3.3%; Score 7; DB 16; Length 101;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 101 ISVAVGL 107
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 DB 73 ISVAVGL 79

Search completed: October 21, 2002, 16:20:46
 Job time : 65 secs